GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Result
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Listing first 45 summaries
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1 MALLTNLLPLCCLAL
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61 GPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPG 120

1 MALLINLLPLCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGAS 60 MALLINLLPLCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGAS 60

Query Match 100.0%; Score 2088; DB 1; Best Local Similarity 100.0%; Pred. No. 1.1e-216; Matches 396; Conservative 0; Mismatches 0;

Length 396; Indels

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1  (64; Ax-1999 (first entry) Ax-1999 (first entry) Ax-1999 (first entry) Ax-1999 (first entry) In Desert hedgehog (Dhh) protein. In thedgehog; Dhh protein; human; dopaminerg; therapeutic; patched; signal transduction; lington's disease; amyotrophic lateral sclere bral ischaemia; hypoxia; neuroprotective; tington's disease; amyotrophic lateral sclere spieles.  (0-) ONTOGENY INC. (0-) ONTOGENY INC. (0-) ONTOGENY INC. (1-) 99:142578/12. (1-) 198; W07270. (2-) ONTOGENY INC. (3-) 138pq; K, Wang M; (3-) 242578/12. (3-) 242578	W97767 Y05512 W61486 R77340 R77369 W97769 Y05514 W79597 W79598 W79598 R77343 R17343
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      A new method to regulate muscle growth

25 Disclosure; Page 121-121; 130pp; English.

26 Invention relates to a method for modulating the formation and/or invention relates to a method for modulating the formation and/or maintenance of muscle tissue by ecotopically contacting muscle cells, especially muscle stem/progenitor cells, in vitro or in maintenance of muscle stem/progenitor cells, in vitro or in cells, especially muscle stem/progenitor cells, in vitro or in molecule that mimics the effect of hedgehog porteins on patched signalling, or activates or potentiates patched signalling, or activates or potentiates patched signalling, in an amount effective to alter the growth state of the treated cells.

27 Also claimed is a method for treatment or prevention of disorders of, or surgical or cosmetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be muscle atrophy, in particular skeletal muscle atrophy or cardiac muscle atrophy, cacheaia, or muscular myopathy atrophy or cardiac muscle atrophy, cacheaia, or muscular myopathy atrophy or cardiac muscle atrophy, cacheaia, or muscular myopathy calling portion of myoblastic or neoplastic growth of muscle tissue to provide treatment of hyperblastic or neoplastic growth of muscle tissue such as in myopathy comprises at least a bloactive extracellular portion of a hedgehog protein (see Y05510-19) encoded by a vertebrate hedgehog gene (see X25098-107), especially a human hedgehog gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              74-MAR-1999; U17922.
29-AUG-1998; US-057394.
29-AUG-1997; US-057394.
(ONTO-) ONTOGENY INC.
31adgen CS, Currie PD, Hughes St
WpI; 99-243557/20.
N-PSDB; X25105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ijuman Desert hedgehog protein Dhh.
Desert hedgehog; Dhh protein; human; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
pachexia; muscular myopathy; myoblastic sarcoma; therapy.
Sequence
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MALLTNLLPLCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGAS

Query Match
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Matches 396; Conser

Conservative

100.0%; 0

Score 2088; DB 1; Pred. No. 1.1e-216; ; Mismatches 0;

Indels Length

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MALLINLLPLCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGAS

Query Match
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Claim 4; Page 24-25; 39pp; English.

Claim 4; Page 24-25; 39pp; English.

Chair 1s the amino acid sequence of a precursor of a novel human beart hedgehog protein, as deduced from a cDNA clone (see V62395).

Chair 2d from cell line ARH-77 (ATCC CRL-1621). The mature form clonal antibody (MAD) that recognises the protein, a process for producing the protein, and a method for detecting the protein.

Chair 2d from cell line ARH-77 (ATCC CRL-1621). The mature form concolonal antibody (MAD) that recognises the protein, a process for producing the protein, and amethod for detecting the protein.

Chair 2d for producing the protein, and the MAD is useful for detecting and purifying the protein, and the MAD is useful for detecting and purifying the protein. The hedgehog protein, abnormalities in humans to establish their treatments and diagnoses.

Sequence 396 AA;
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N-PSDB; V62395.
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W79595;
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25-APR-1997; JP-121578.
(HAYB ) HAYASHIBARA SEIBUTSU
Ariyasu T, Nakamura S, Orita
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24-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; monoclonal antibody.
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                                                                                                                                                                                                                                                                                              KAGAKU
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                                                                                                                                                                                                                            corresponding DNA
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                                                 Query Match
Best Local S
Matches 382
                                                                                                                                        Claim 17; Page 135-37; 210pp; English.

The sequence represents a mouse Indian hedgehog protein, homologout to a Drosophila hedgehog protein (R77337), and is encoded by a cDN isolated by low stringency screening of a mouse genome DNA library probes and primers derived from hedgehog sequences may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy.

Antibodies generated from the protein may be used as therapeutic c
                                                                                                                                                                                                                                  Claim 17; Page 135-37;
                                                                                                                                                                                                                                                                                      Ingham PW, Mcmahon WPI; 95-255060/33. N-PSDB; Q91642.
                                                                                                                                                                                                                                                                                                                              (HARD )
                                                                                                                                                                                                                                                              Hedgehog-like protein(s) and nucleic acid(s) encoding them - useful to treat degenerative nervous system disorder(s) and in gene
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                         30-DEC-1993;
14-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nervous system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1996 (first entry)
Mouse desert hedgehog protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R77345 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
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MALPASILPICCIALIAISAQSCGPGRGPVGRRRYVRKQIVPILIKQFVPSMPERTIGAS 60
                        MALLTNLLPLCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGAS 60
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-1993; US-176427.
-1994; US-356060.
) HARVARD COLLEGE.
) IMPERIAL CANCER F
                                                             Similarity
                                                                                                                  reagents.
                                                 96.2%;
nilarity 96.5%;
Conservative
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Tabin CJ;
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                                                 Score 2008; D
Pred. No. 4.5e
6; Mismatches
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                                                  4.5e-208;
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library.
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                        Pri Method for limiting damage to neurons caused by ischaemic or epoxic pri conditions - is used for the treatment and prevention of e.g. conditions - is used for the transient ischaemic or epoxic pri cerebral infarction, stroke and transient ischaemic attacks Disclosure; page 65-66; 104pp; English.

CC A method has been developed for limiting the damage to neuronal cells by cischaemic or epoxic conditions by administering a ptc (patched); cc construct which recombines with the genomic hedgehog gene to provide a cc neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a cc erebral tissues against ischaemic linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect construct transcription regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect compania, stroke (thrombolic or embolic) and transient ischaemic conjunction of the brain or spinal cord, oedema caused by trauma, haemorrhage can dencephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons cue to oxygen depletion, including in patients with hypotension. The creatment reduces cIV by at least 25, particularly at least 70,%. The coronarion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Dhh hedgehog protein sequence.
Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell;
brain infarction; cerebral infarction; transient ischaemic attack;
stroke; cerebral infarct volume; spinal cord; oedema; trauma;
haemorrhage; encephalomyelitis; coronary bypass; cerebral hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mahanthappa NK;
WPI; 99-095458/08.
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27-JUN-1997; US-883656.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVL
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Query Match
Best Local Similarity
Matches 382; Conserv

Conservative

96.2%;

Score 2008; DB 1; Pred. No. 4.5e-208; 6; Mismatches 8;

Length

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PT increasing the survival of neuronal, dopaminergic and GABA-nergic PT cells - by using a ptc therapeutic such as a protein kinase pt inhibitor, or an agent derived from hedgehog polypeptides, useful in PT inhibitor, or an agent derived from hedgehog polypeptides, useful in PT the treatment of Parkinson's disease

CC Disclosure; Page 85-86; 138p; English.

CC Invention is based on the finding that hedgehog protein (Dhh). The cc invention is based on the finding that hedgehog proteins are useful CC as protective agents in the treatment and prophylaxis of neurodegenerative disorders resulting from the loss of dopaminergic conducts of GABA-nergic neurons, or the general loss of tissue from the substantia nigra. Exemplary disorders include Parkinson's disease, CC und cerebral ischaemia. The invention relates to hedgehog constructs encoding recombinant hedgehog polypeptides and CC rans activation constructs for altering hedgehog polypeptides and CC as constructs for altering hedgehog gene regulatory constructs of naturally occurring hedgehog proteins on patched signalling) CC and Dhh polypeptides (see W97763-64) are preferred. The products can also be used for the maintenance of differentiated neurons in CC and animal. They can be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-1999.
24-JUL-1998; U15419.
24-JUL-1997; US-900220.
(ONTO-) ONTOGENY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Desert hedgehog (Dhh) protein.

Desert hedgehog; Dhh protein; mouse; dopaminergic; GABA-nergic; ptc therapeutic; patched; signal transduction; Parkinson's dise Huntington's disease; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 99-142578/12.
N-PSDB; X07272.
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A new method to regulate muscle growth

St Disclosure; Page 112-113; 130pp; English.

Creating method to regulate muscle growth

Creating method read the sequence is mouse Desert hedgehog protein Dhh. The

Creating muscle tissue by ecotopically contacting muscle

Creating especially muscle stem/progenitor cells, in vitro or in

Creating especially muscle stem/progenitor cells, in vitro or in

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Best Local Similarity
Matches 382; Conser
                                                                                                                                                                                                                                                                                                                                                                        04-MAR-1999; U17922.
28-AUG-1998; U17922.
29-AUG-1997; US-057394.
(ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hughes Sh
WPI; 99-243557/20.
N-PSDB; X25099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prevention and/or treatment of hypoxia,
agent.
Sequence 396 AA;
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Desert hedgehog; Dhh protein; mouse; hedgehog therapeutic; ptc therapeutic; patched; signal transduction; muscle atro
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                                                                                                                                                                                                                                                                                                                                                                                  24-APR-1998;
14-APR-1998;
25-APR-1997;
                                                                                                                                                                                                       antibody Claim 3;
This is the amino acid sequence of a precursor of a novel human Desert hedgehog proteen, as deduced from a CDNA clone (see V62394) derived from cell line ARH-77 (ACC CRL-1621). The mature form (see W7959) of the hedgehog protein is also claimed, as are a monoclonal antibody (MAb) that recognises the protein, a process for producing the protein, and a method for detectin, a process for producing the protein, and a method for detecting the protein. The hedgehog protein is useful in establishment of hybridomas which produce antibodies recognising the protein, and the MAb is useful
                                                                                                                                                                                                                                                      Human Desert hedgehog
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Ariyasu T, Nakamura S, Orita
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Best Local
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13-JUL-1995.
30-DEC-1994; U14992.
30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
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Claim 17; Page 139-41; 210pp; English.

The sequence represents a mouse sonic hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and is encoded by a cDNA isolated from an 8.5-day post coitum mouse library. Probes and primers derived from the sonic hedgehog
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               Method for limiting damage to neurons caused by ischaemic or epoxic conditions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks Disclosure; Page 68-70; 104pp; English.

A method has been developed for limiting the damage to neuronal cells ischaemic or epoxic conditions by administering a ptc (patched) therapeutic agent to reduce cerebral infarct volume (CIV). Damage to neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic hedgehog gene to provide a second construct which recombines with the genomic second construct which recombines which recombines which recombines which recombines which recombines w
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Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell brain infarction; cerebral infarction; transient ischaemic attack; stroke; cerebral infarct volume; spinal cord; oedema; trauma; stroke; cerebral infarct volume; spinal cord; oedema; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used gene therapy. Antibodies generated from the protein may be used as therapeutic or research reagents.

Sequence 437 AA;
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29-APR-1999 (first entry)
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WPI; 99-095458/08.
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27-JUN-1997; US-883656.
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W09904775-A2.
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24-JUL-1998; U15419.
24-JUL-1997; US-900220.
(ONTO-) ONTOGENY INC.
Mahanthappa NK, Miao N, 1991; 99-14257812.

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Increasing the survival of neuronal, dopaminergic and GABA-nergic cells - by using a ptc therapeutic such as a protein kinase

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Best Local Similarity
Matches 249; Conser
                                                                                                                                                                                                                                                                                                                       21-MAY-1999 (first entry) mouses sonic hedgehog (Shh) protein. Sonic hedgehog; Shh protein; mouse; dopaminergic; GAI sonic hedgehog; Shh protein; mouse; dopaminergic; GAI ptc therapeutic; patched; signal transduction; Parkir Huntington's disease; amyotrophic lateral sclerosis; cerebral ischaemia; hypoxia; neuroprotective; therapy
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Pred. No. 9.6e-123
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RESULT
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Disclosure; Page 89-91; 138pp; English.
This polypeptide is mouse shh Sonic hedgehog protein. The invention is based on the finding that hedgehog proteins are useful. Can protective agents in the treatment and prophylaxis of cheurodegenerative disorders resulting from the loss of tissue from the substantia nigra. Exemplary disorders include parkinson's disease, thuntington's disease (both claimed), amyotrophic lateral sclerosis and cerebral ischaemia. The invention relates to hedgehog constructs therapeutics (i.e. hedgehog polypeptides and gene therapy constructs therapeutics on constructs for altering hedgehog gene regulatory sequences) and ptc therapeutics (i.e. agents which mimic the effect of naturally occurring hedgehog proteins on patched signalling) constructs (see w97763-64) are preferred. The products and be used for the maintenance of differentiated neurons in cultures, and to enhance the implantation of such neuronal cells in the products arising from the use of certain drugs, and in the prevention and/or treatment of hypoxia, e.g. as a neuroprotective agent.
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Matches
05-JUL-1999 (first entry)
Mouse Sonic hedgehog protein Shh.
Sonic hedgehog; Shh protein; mouse; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy.
                                                                                                                                           Y05513 standard; Protein; 437 Y05513;
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llarity 58.7%;
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W0991004-A2.
W0991004-A2.
04-MAR-1999.
28-AUG-1998; U17922.
29-AUG-1997; US-057394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Also claimed is a method for treatment or prevention of disorders of, or surgical or cosmetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be muscle atrophy, in particular skeletal muscle atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy (all claimed). The hedgehog polypeptide or ptc therapeutic can inhibit growth of myoblastic-derived tissue to provide treatment of hyperblastic or neoplastic growth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at least a bloactive extracellular portion of a hedgehog protein (see Y05510-19) encoded by a vertebrate hedgehog gene (see X35098-107), especially a human hedgehog gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A new method to regulate muscle growth Disclosure; Page 115-116; 130pp; English.

The present sequence is mouse Sonic hedgehog protein Shh. The invention relates to a method for modulating the formation and, maintenance of muscle tissue by ecotopically contacting muscle
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Bladgen CS, Currie PD,
WPI; 99-243557/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene (see
Sequence
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Pred. No. 9.6e-123;
3; Mismatches 82;
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PT claim gene(s)

PS claim 13; Pages 153-154; 210pp; English.

CC This represents a mouse sonic hedgebog (shh) protein sequence. The CLAIM 13; Pages 153-154; 210pp; English and compounds for modulating proliferation or CC differentiation of neuronal cells, cholesterol biosynthesis or transport in a cell comprises contacting a CC cholesterol biosynthesis or transport in a cell comprises contacting a CC collesterol biosynthesis or transport in a cell comprises contacting a CC cell with a compound that affects hedgehog, thereby affecting cholesterol biosynthesis or transport. The methods for inhibiting the neural inducing cell with a compound that affects hedgehog, thereby affecting cholesterol biosynthesis or transport. The methods for inhibiting the neural inducing cativity of a hedgehog polypeptide in cells, and for inducing pituitary gland gene expression utilises sequences selected from a zebrafish compound that hedgehog (twhh) protein (W61485), a zebrafish sonic hedgehog (shh) protein (W61486), a chicken shh protein (W61487) or a mouse shh protein (W61488). The products and methods provide for compounds which can affect hedgehog activity. They can be used for treating disorders which arise from neuronal degeneration or abnormal function. They can calso be used as nerve-sparing agents or in restoring or promoting can also be used for treating during the healing of major limb trauma. They can also be used for treating Smith-Lemii-Optiz syndrome. The products can
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Best Local Similarity
Matches 248; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
W09830576-A1.
16-JUL-1998.
17-JUL-1998.
18-JUS-1997; U15753.
18-JUS-1997; U5-061323.
18-JUS-1997; US-061323.
18-JUS-1997; US-081323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New hedgehog-derived poly:peptide(s) - used to develop products modulating proliferation or differentiation of neuronal cells, cholesterol biosynthesis or transport or expression of pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse sonic hedgehog (shh) protein.
Hedgehog polypeptide; neuronal cell proliferation; zebrafish; shh;
cholesterol blosynthesis; pituitary gland gene expression; mouse;
tiggy-winkle hedgehog protein; twhh; sonic hedgehog; major limb trauma;
neuronal degeneration; nerve-sparing agent; Smith-Lemli-Optiz syndrome.
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                                                                                                                                                                                                                                                                                                                                     RLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNH 181
                                                                                                                                                       FLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA----RGPAPAPGDFAPVFARRLRAG 297
                                                                                                                                                                                                                                             VHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLL 241
                                                                                                                                                                                                                                                                                                                                                                                                  RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNWWPGV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLPLCCLALLA-----LPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASG 61
AHRAFAPLRLLHA-LGALLP--
                                            QRVYVVAERGGDRRLLPAAVHSVTLREEEAGAYAPLTAHGTILINRVLASCYAVIEEHSW
                                                                   DSVLA---PGGD-ALRPARVARVA-REEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQW 352
                                                                                                                                                                                                                        IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT
                                                                                                                                                                                                                                                                                                                KLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAH
                                                                                                                             FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGP---SALFASRVRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLARCFLVILASSLLVCPGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTLGASG 61
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Pred. No. 2e-122;
4; Mismatches 8
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-GGAV--
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---QPT-GMHWYSRLLYRLA 391
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Best Local
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Claim 17; Page 133-35; 210pp; English.

The sequence represents a chicken sonic hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and is encoded by a cDNA isolated from a stage 22/22 limb bud cDNA library. Probes and primers derived from the sonic hedgehog gene may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the protein may be used as therapeutic or research reagents.

Sequence 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicken sonic hedgehog protein.

Chicken; sonic hedgehog protein; stage 22/22 limb bud; probe; primer; diagnostic; nervous system disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUL-1995.
30-DEC-1994; U14992.
30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hedgehog-like protein(s) and nucleic to treat degenerative nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 95-255060/33.
N-PSDB; Q91636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HARD ) HARVARD COLLEGE.
(IMCR ) IMPERIAL CANCER RES TEINGHAM PW, MCMAhon AP, Tabin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus
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R77338;
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                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                      μ
                                                                                                  DFLTFLDRMDSSRKLFYVIETRQPRARLLLTAAHLLFVAPQHNQSEATGSTSGQALFASN
                                                                 SRNHVHVSVKADNSLAVRAGGCFFGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPT
                                                                                                                                                                  GASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMMM 117
                                                                                                                                                                                                                                   MALLTNLLP----LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL
                       PVLLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA--RGPAPAPGDFA--PVFARR
                                                SKAHIHCSVKAENSVAAKSGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYS
                                                                                                                                                                                                            MLLLTRILLVGFIC - - ALLVSSGLTCGPGRG - IGKRRHPKK - LTPLAYKQFIPNVAEKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domesticus.
                                                                                                                                                                                                                                                             57.4%;
ilarity 59.4%;
Conservative 5
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27. .3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TECHNOLOGY
                                                                                                                                                                                                                                                          Score 1198; DB 1;
Pred. No. 1e-120;
"'Amatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence (R77349)"
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DR WPI; 99-095458/08.

DR WPIS; 99-095458/08.

DR N-BSDB; X16182.

PT Method for limiting damage to neurons caused by ischaemic or epoxic PT conditions - is used for the treatment and prevention of e.g.

PT Method for limiting damage to neurons attacks

PT cerebral infarction, stroke and transient ischaemic attacks

PS Disclosure; Page 63-64; 104pp; English.

CC A method has been developed for limiting the damage to neuronal cells by cischaemic or epoxic conditions by administering a ptc (patched)

CC therapeutic agent to reduce cerebral infarct volume (CIY). Damage to construct which recombines with the genomic hedgehog gene activation construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a customatic transcription regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect cerebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic construct with based as a prophylactic in many other cases of injury to the brain or spinal cord, codema caused by trauma, haemorrhage and tenephalomyelitis, or in conjunction with (coronary bypass) surgery.

CC reatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The coronarion coronarion coronarion with protection.

CC invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 59.4
Matches 244; Conservative
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07-JAN-1999.
26-JUN-1998; U13387.
27-JUN-1997; US-883656.
(ONTO-) ONTOGENY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken Shh hedgehog protein sequence.

Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell brain infarction; cerebral infarction; transient ischaemic attack; stroke; cerebral infarct volume; spinal cord; oedema; trauma; haemorrhage; encephalomyelitis; coronary bypass; cerebral hypoxia.
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SRNHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPT 237
|: |:| |||:| :| :| || || ||::::
SKAHIHCSVKAENSVAAKSGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYS 239
                                                                                                                                                 GASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNM 117
||| ||:: | |||::| ||||||||||||:|||::||||::|||||:|||
GASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQ 119
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Search completed: June 5, 2000, 08:16:20 Job time: 2585 sec

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Result
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Maximum DB seq
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Listing first 45
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1285
1263.5
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Gapop 10.0 , Gapext 0
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Copyright (c) 1993 - 2000 Comp
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sp_unclassified:*
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sp_virus:*
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1 Q9WUP6
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Q9w6c1 eleutheroda
Q9ygy7 ambystoma m
O96699 junonia coe
Q9wup6 rattus norv
O42128 oryzias lat
Q9ygu3 brachydanio
O42441 oryzias lat
O42234 coturnix co
P91573 caenorhabdi
O9xv14 caenorhabdi
O9xv12 caenorhabdi
Q9xv2 caenorhabdi
Q9xv2 caenorhabdi
                                                                                                                                                                                                                                                                                          057567 notophthalm
057404 pleurodeles
Q9w7q9 paralichthy
073803 fugu rubrip
017499 branchiosto
061676 lytechinus
                                                                                                                                                                                                                                                   Q9xsi6 bos taurus
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                                                                                                                                                                                                                                                                    09wv29 rattus norv
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O57567
ID 05766
AC 055
AC 050
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SEQUENCE FROM N.A.

STARK D.R., GATES P.B., BROCKES J.P., FI
Dev. Dyn. 0:0-0(1998).

EMBL; AF047466; AACO3108.1; -.

HSSP; Q62226; IVHH.

BFAM; PF01079; HH\_Signal; 1.

PFAM; PF01079; Hint; 1.

PRINTS; PR00632; SONICHHOG.

SEQUENCE 406 AA; 45072 MW; 9DOFFA76

9D0FFA76 CRC32;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
94.5	95	95	95	UЛ	95.5	96	σ.	96.5	97	97	86	98.5	99	100.5	102	105	123.5	138.5	138.5	140	148	148.5	154.5	161
4.3	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	5	4 5	4.5	4.5	4.6	4.6	4.7	4.8			6.4	6.4	6. 8	6.8	7.1	7.4
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Q9Y2U4	Q9Z4Z9	P96285	Q50470	053152	Q9Y6K2	Q54297	039278	042233	Q9Z4X6	Q14160	Q9YC75	Q9ZBV4	053499	043955	Q21754	005647	Q23193	045273	Q94130	Q94129	Q94128	045992	Q21535	Q21835
Q9y2u4 homo sapien		P96285 mycobacteri		O53152 mycobacteri	Q9y6k2 homo sapien	S	039278 equine herp	ω		homo sapie			O53499 mycobacteri	043955 leishmania		O05647 streptomyce	Q23193 caenorhabdi		Q94130 caenorhabdi		Q94128 caenorhabdi	045992 caenorhabdi	Q21535 caenorhabdi	Q21835 caenorhabdi

## ALIGNMENTS

O57567 PRELIMINARY; PRT; 406 AA. 057567; 01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last annotation update) HEDGEHCG SEGMENT POLARITY HOMOLOG.

Notophthalmus viridescens (Eastern newt) (Triturus viridescens). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus

FERRETTI P.;

Db Oy	Qу	Db Qy	Db Qy	Que Bes Mat
198 194	138 134	78 74	18 15	Query Match Best Local Matches 29
AKTG	HHSE	FKEL 	111     	atch cal S 292
GCFP1  - -  GCFP1	ESLH!      ESLH!	TPNYI      TPNYI	VPAAI     GPGAI	imila ; Co
AGAQV ARALA	EGRA EGRA	APDII	1006b	Query Match Best Local Similarity Matches 292; Conserv
RLESG      TLESG	VDITI	FKDEE FKDEE	GRVVG    :  GRVIG	70 74 vativ
ARVAI ;; EKIP;	SDRDI	NTGAI	SRRRI       RRPRI	e . 1 . 8
SAVR : : [ADLE	NKYG 	DRLMT   :   DRIMT	PRKL	Sco Pre
PGDRV 	LLARI :     MLARI	QRCKD       QRCKD	VPLAY    :   IPLSY	Query Match 70.8%; Score 1539; DB 13; Best Local Similarity 74.1%; Pred. No. 2.2e-117; Matches 292; Conservative 31; Mismatches 69;
LAMGE 	AVEAC      AAEAC	RLNSI 	KOFSI	39; 1. 2.1
EDGSP     EGGRR	SEDWV	AISV	ONVPE  :	DB 1 2e-11
TFSDV  :   TYSDE	YYESH       YYESH	ANOME	KTLG!       KTLG!	
198 AKTGGCEPAGAQVRLESGARVALSAVRPGDRVLANGEDGSPTESDVLIFLDREPHRLRAF 257	138 HHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHSAA 197    :	78 FKELTDNYNDDIIFKDEENTGADRIMTQRCKDRINSLAISVANQWPGVKLRVTEGWDEDG 137 	18 LLLVVPAAWGCGFGRVVGSRRRPPRKLVPLAYKOFSPNVPEKTLGASGRYEGKIARSSER 77 	Length 406; Indels 2
DREPH   : DRDST	CSVKS	RVTEG       RVTEG	EGKIA 	406
RLRAE ::   AVKEE	EHSA	WDEDC	RSSEI  :   RNSEI	); 2; Gaps
257	197	137	R 77	aps
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RESULT
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Matches 255
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMIT X., NICOLAS S., LE PARCO Y.
SUBMITCHED (MAY-1997) to the EMBL/G
EMBL; AF003532; AAB94412.1; -.
4 EMSP; 060226; 1VHH.
EMSP; 060226; 1VHH.
R PFAM; PF01005; H1signal; 1.
R PFAM; PF01079; Hint; 1.
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O57404;
O57404;
O57404;
O57404;
O1-UN-1998 (TrEMBLrel. 05, Created)
O1-UN-1998 (TrEMBLrel. 06, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SONIC HEDGEHOG-RELATED PROTEIN.
  Q9W7Q9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Caudata; Salamandroidea; Salamandridae; Pleurodeles
                                                                                                                       378
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                                                                                                                       GFGILSFFSPQDYSSHSPPAPSQAEGVHWYSEILYRIGTWVLQADTIHPLGMAAKSS
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Similarity 61.7
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  PRELIMINARY;
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Pred. No. 1.1e
46; Mismatches
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Best Local Sim
Matches 251;
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073803;
01-AUG-1998 (TIEMBLIEL O
01-AUG-1998 (TIEMBLIEL O
01-NOV-1999 (TIEMBLIEL O
FUGU HEDGEHOG.
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01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
SONIC HEDGEHOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE: 99238226.
SUZUKI T., ICHIRO O., KU
"Retinoic acid given at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHH.
Paralichthys olivaceus (Flounder).
Paralichthys olivaceus (Flounder).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Neopterygii; Teleostei; Euteleostei; Bothidae; Paralichthys.
            SEQUENCE FROM N.A.
GELLNER K., BRENNER S.;
Submitted (MAR-1998) to
                                                                                                                           FHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Retinoic acid given at late embryonic stage depresses sonic hedgehog and Hoxd-4 expression in the pharyngeal area and induces skeletal malformation in flounder (Paralichthys olivaceus) embryos."; Dev. Growth Differ. 41:143-152(1999).

EMBL; AB029748; BAA82360.1; -.
                                                                  Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebratta; Actinopterygil;
Neopterygil; Teleostei; Euteleostei; Acanthopterygil; Percomorpha;
Tetraodontiformes; Tetraodontoidel; Tetraodontidae; Fugu.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLLLVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGKIARSS
                                                                                                                                                                                                                                                                          LFSSQPQASAQKDGVHWYSKILYQLGTWLLDSHSIHPLGMS
                                                                                                                                                                                                                                                                                                                                                                                 LFYVIET-DSGQKITLTAAHLLFVGHSNSTERAHRGMSAVFASQVRPGQTVFVLDAERLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         VAAKSGGCFPGSSTVTLQDGTKKPVKALQTGDRVLAADAHGQPVYTDFIMFIDQDSTTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGHHFEESLHYEGRAVDITTSDRDKSKYGTLSRLAVEAGFDWVYYESKAHIHCSVKAENS
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 AF056116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 58.1%;
Similarity 62.6%;
51; Conservative '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
99238226.
C., ICHIRO O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 AA;
1998) to the AAC34384.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45945 MW;
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Last sequence up
Last annotation
                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score 1263.5; DB 13
    Pred. No. 5.6e-95;
17; Mismatches 92;
            EMBL/GenBank/DDBJ
                                                                                                                                                                            Created)
                                                                                                                                                                                                         PRT;
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Best Local Sim
Matches 225;
                              Query Match
Best Local S
Matches 215
                                                                              EMBL; Y13858; CAA74169.1;
HSSP; Q62226; 1VHH.
PFAM; PF01085; HH_signal; 1.
PFAM; PF01079; Hint; 1.
PRINTS; PR00632; SONICHHOG.
SEQUENCE 415 AA; 46765 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q62226; 1VHH.
PFAM; PF01085; HH_si
PFAM; PF01079; Hint;
SEQUENCE 442 AA;
                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                          SHIMELD S.M.;
Submitted (JUN-1997)
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                     Branchiostoma.
                                                                                                                                                                                             Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                   AMPHIHH
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                                                                                                                                                                                                                                                                                                                                              LLLEEGSFHP 403
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                              Similarity 53.3
15; Conservative
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                                                                                                                                                                                                                                                                               PRELIMINARY;
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; Hint; 1.
2 AA; 49286
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Pred. No. 1.5e
54; Mismatches
                             Score 1076.5; DB 
Pred. No. 9.1e-80; 
6; Mismatches 127
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1.5e-80;
nes 98; I
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Best Local Similarity
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Submitted (APR-1998) to the EMB:
EMBL; AF059606; AAC15065.1; -.
HSSP; Q62226; IVHH.
PFAM; PF01079; Hint; 1.
PFAM; PF01079; Hint; 1.
PRINTS; PR00632; SONICHHOG.
SEQUENCE 410 AA; 46071 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           061676;
061676;
01-AUG-1998
01-AUG-1998
01-NOV-1999
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Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae; Lytechinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEGWDEDGFHTEESLHYEGRAVDITTSDRDRTKYGMLARLAVEAGFDWVYYESKAHIHCS
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                                                                                                       RSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEG
                                                                                                                                                                                                            CLIAL-----TQACHPGR-SGKTSHRPRNRTPLQYKQKVPNISEDTFGÅSGPPEGRID
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DSTLFYVIETED-KTIVQLTPQHLIYVSERESN-FDQSRAVFASEVRTNQFVYTTAQNHD
                                                   ESAAAKNSGGCFPGFSQAYLKNGRMISMLDIRVGDEVAVVNNNGELDYSDVIMIVHRKLN
                                                                 EHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREPH
                                                                                                                                                          RDDERFSKLSPNNNDDIVFKDEEGTGADRLMTQRCKDKLNTLAISVMNEWPGIKLRVVEA
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                         RLRAFQVIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQPGQYVLVAGV---
                                                                                                                                                                                                                                                                      192;
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(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                   42.0%; Score 914; DB 5;
48.2%; Pred. No. 1.5e-66;
tive 62; Mismatches 124
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                     Q9XS16
Q9XS16;
Q9XS16;
Q1-NOV-1999 (TrEMBLrel. 12, C)
Q1-NOV-1999 (TrEMBLrel. 12, Le
Q1-NOV-1999 (TrEMBLrel. 12, Le
SONIC HEDGEHOG (FRAGMENT).
                KOYAMA E., IWAMOTO M., OHMORI T., KURISU K., WU C., OO BASHIR M.M., TUCKER T., PACIFICI M.;
"Development of Stratum Intermedium and its Role as a Signaling Structure During Odontogenesis.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ database EMBL; AF144100; AAD33926.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9WV29
O9WV29;
O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
INDIAN HEDGEHOG PROTEIN (FRAGMENT).
                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
Eutheria; Cetartiodactyla; Run
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Rodentia; Sciurognathi; Muridz
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                           Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARGES P.L., MEYER R.A. JR., "Indian hedgehog in rat.";
Submitted (JUN-1999) to the E EMBL; AF162914; AAD45372.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY; GARGES P.L., MEYER R.A. JR., BROWN C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                           TISSUE-TOOTH GERM;
                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                               222
                                                                                                                                                                                                                                                                                                                                                             162
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                                                                                                                                                                                                                                                                                      LMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRN 161
                                                                                                                                                                                                                                                                                                                                                                                 LMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISHMLGITDTDTGQEQRVHWYTQGLYKLGKYVMSDRLF 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --HSLAWGSWTPG--EGVHWYPQLLYRLGRLLLEEGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGLQPARVAAVSTHVALGAYAPLIKHGILVVEDVVASCFAAVADHHLAQLAFWPLRLF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGVRPMKVVSVTTRLGHTAVAPVTRQGSLVIDGVAVSSYAVMRDEWVAHASFAPIRWYTY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
177
177
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19739 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        41.6%;
96.6%;
                                                                                                                                      ta; Craniata; Vertebrata; Mammalia;
Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 904; DB
Pred. No. 2.9e
4; Mismatches
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                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muridae;
                                                                                                                                                                                                                                 139
                                                                                                                                                                                                                                                                                                                                                                                                                    2.9e-66;
2.3e-66;
2;
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ae; Murinae;
                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICE D.K.;
                                                                                                                                                                                  update)
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                                  databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Rattus.
                                                                               OOKURA
                                                        Sonic Hedgehog-
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RESULT
Q9YGV7
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Q9W6CL1

ID W6CL1

ID W6CL

ID CO

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Best Local S
Matches 125
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Best Local S
Matches 129
                                        Q9YGV7
Q9YGV7;
Q9YGV7;
01-MAY-1999 (TrEMBLrel. 10, 0
01-MAY-1999 (TrEMBLrel. 10, 1
01-NOV-1999 (TrEMBLrel. 12, 1
SONIC HEDGEHOG (FRAGMENT).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  direct developing frog E. coqui.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF113403; AAD23436.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eleutherodactylus coqui.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Neobatrachia; Bufonoidea; Leptodactylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9W6C1 PRELIMINARY; PRT; 138 AA.
Q9W6C1;
Q9W6C1;
O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SONIC HEDGEHOG PROTEIN (FRAGMENT).
                       Ambystoma mexicanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Differences in vertebrate limb
                                                                                                                                                                                                                                                                                                  174 GFDWVYYESKAHVHCSV 190
                                                                                                                                                                                                                                                                                                                                                                                                               114
                                                                                                                                                                                                                                                                               122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108
                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Sir
hes 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
mes 125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
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                                                                                                                                                                                                                                                                             GFDWVYYESKAHIHCSV 138
                                                                                                                                                                                                                                                                                                                                                               KDRLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLA 167
||:||:||:|||:||:||:||:||:||:||:||
KDKLNALAISVMDQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYKQFSPNVPEKTLGASGRYEGKIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLAVEAGFDWVYYESKAHI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLAVEAGFDWYYYESKAHV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYKQFIPNVAEKTLGASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRC
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138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RICHARDSON M.K.,
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15751 MW;
                         (Axolotl)
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                                                                  Created)
Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 681; DB 13;
Pred. No. 2.8e-48;
7; Mismatches 5;
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Pred. No. 6.7e-50;
Craniata;
                                                                                                                                                           PRT;
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Vertebrata; Amphibia;
                                                                                                                                                           A
                                                               on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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SOFFICERRE

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Query Match
Best Local Similarity
Matches 123; Conserv
                                                                                                                         Query Match
Best Local
                                                                                                                Matches
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOROK M.A., IZPIZUA-BELMONTE J.C., GARDINER D. Submitted (OCT-1997) to the EMBL/GenBank/DDBJ EMBL; AF031480; AAD18128.1; -. HSSP; Q62226; 1VHH. 1
                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                             Junonia coenia (Peacock butterfly) (Precis coenia).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                 HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                 096699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Batrachia; Caudata;
                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                               Science
                                                                                                                                                                                                                        evolution.";
                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                               Recruitment of a hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                        208 AQVRLESGARVALSAVRPGDRVLAMGEDG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148
123
                  183
                                                      123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GRAVDITTSDRDRSKYGMLARLAVEAGFDWYYFESKAHIHCSVKAENSVAAKSGGCFPAS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
                                     63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | GRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHSAAAKTGGCFPAG
                                                                                                                                                                                         nce 0:0-0(1999).
; AF117742; AADO:
; Q62226; 1VHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYE
                                   DIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYE
                                                                                  ASGRYEGKIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQW 122
                                                                                                                                                                                                                                                                                                                                                                                                                              AKVTLEHGVTRPVKDLRPGDRVLAADGQG 149
RSYIHCSVKTESSVG--TGAGCFPSGAVVHTENGP-XDIASLKKGNKVLA 169
                                                                         ASGPPEGRITRDDEKFRDLVPNYNPDIDFKDDEGTGADRLMTQRCKEKLNTLAISVMNQW 62
                 KAHVHCSVKSEHSAAAKTG-GCFPAGAQVRLESGARVALSAVRPGDRVLA 231
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150
150 AA;
                                                                                                                                                             185
185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                     AAD08931.1;
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16599
                                                                                                                                                                        185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salamandroidea; Ambystomatidae; Ambystoma
                                                                                                                      27.4%;
                                                                                                                                                              20745 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.6%;
                                                                                                                                                                                                                               SELEGUE J.E., PEARSON B.J., SCOTT M.P., CARROLL S.B.; ehog regulatory circuit in b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update
                                                                                                               Score 597; DB : Pred. No. 2.9e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 665; DB 13;
Pred. No. 6.3e-47;
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9356329B CRC32;
                                                                                                                                                              96A09B5A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                185
                                                                                                               .9e-41;
les 25;
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                                                                                                                                Length 185;
                                                                                                                                                                                                                               butterfly eyespot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 150;
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                   GOODRICH L.V.,
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Best Local
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NON_TER
SEQUENCE
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                                                                                                                ARAKI K.;
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ (EMBL; AF148226; AAD31927.1; -...
NON_TER 129 129
SEQUENCE 129 AA; 14570 ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9WUP6;
Q9WUP6;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                               042128
042128;
01-JAN-1998
01-JAN-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Futheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorpha; Cyprinodontiformes; Adrianichthyoidei; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                             Submitted (SEP-1997) to the EMBL; AB007129; BAA22368.1; HSSP; Q62226; IVHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                        STRAIN-BBRR;
                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                        Oryzias latipes (Medaka fish).
                                                                                                                                                                                                                                                                                                                                   SHH, PARTIAL
                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGRAV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGPGRGPVGRRRYVRKQLVPLLYKQFVPSMPERTLGASGPAEGRVTRGSERFRDLVPNYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91;
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                                        Similarity 70.6
84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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119 /
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(TrEMBLrel. 12, Last se
(TrEMBLrel. 12, Last an
EHOG PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                   (TIEMBLrel. 05, Created)
(TIEMBLrel. 05, Last sequence update)
(TIEMBLrel. 12, Last annotation updat

COS (FRAGMENT).
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TISSUE-WHOLE EMBRYO;
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119
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70.6%;
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                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 510.5; DB 11;
Pred. No. 1.9e-34;
0; Mismatches 13;
                                        Score 472; DB 13;
Pred. No. 2.3e-31;
7; Mismatches 18;
                                                                                                            1CAE5021 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129
                                                                                                                                                                                                                                                                                                                                                                                                        119
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RESULT
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ID 22
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Best Local S
Matches 73
                                                                                                                                                                                                                                                                                                                                                                                                                042441 PRELIMINARY; PRT; 80 AA.
042441;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SONIC HEDGEHOG (FRAGMENT).
Oryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorpha;
Cyprinodontiformes; Adrianichthyoidei; Adrianichthyidae; Oryzinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
       NON_TER
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSTLETHWAIT J.;
"Zebrafish hox clusters and vertebrate genome evolution.";
Science 282:1711-1714(1998).
EMBL; AF071236; AAD15931.1; -.
EMSP; Q62226; 1VHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9YGU3;
01-MAY-1999
                                                                                                                     EMBL; Z97019; CAB09695.1; -. HSSP; Q62226; 1VHH. PFAM; PF01085; HH_signal; 1.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.

KOESTER R., STICK R., LOOSLI F., WITTBRODT J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 99051425.

AMORES A., FORCE A., YAN Y.-L., WANG Y.-L., FRITZ A., PRINCE V.,
HOR., AMEMIYA C., LANGELAND J., WESTERFIELD M., EKKER M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DESERT
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01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSVKAESSVAAKSGGCFPGSSTVTLENGTQRPVKDLQPGDRVLAADYDGNPVYTDFIMF 119
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       80
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9180 MW;
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10, Last sequence update)
12, Last annotation update)
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Pred. No. 1.9e-25;
5; Mismatches 10;
           59BE42B8 CRC32;
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Matches
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              153
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ITTSDRDKSKYGTLSRLAVE 80
        ITTSDRDRNKYGLLARLAVE
                                                           17.9%;
l Similarity 90.0%;
72; Conservative
              172
                                                           Score 389; DB 13;
Pred. No. 7.3e-25;
5; Mismatches 3
                                                                          Length 80;
                                                            Indels
                                                            0
                                                           Gaps
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Search completed: June 5, 2000, 08:19:30 Job time: 184 sec

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Result
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Maximum DB seq
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Query Match
Best Local Similarity 100.

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                                                                                                                                                                               Increasing the survival of neuronal, dopaminergic and GABA-nergic recils - by using a ptc therapeutic such as a protein kinase rinhibitor, or an agent derived from hedgehog polypeptides, useful in the treatment of parkinson's disease. Scalaim 30; Page 95-97; 138pp; English.

This polypeptide is human Indian hedgehog protein (Ihh). The protective agents in the treatment and prophylaxis of an eurodegenerative disorders resulting from the loss of dopaminergic and/or GABA-nergic neurons, or the general loss of tissue from the cubertal and/or GABA-nergic neurons, or the general loss of tissue from the substantia nigra. Exemplary disorders include Parkinson's disease, and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene therapy constructs e.g. constructs encoding recombinant hedgehog gene regulatory constructs for altering hedgehog gene regulatory sequences) and ptc therapeutics (i.e. agents which mimic the effect of naturally occurring hedgehog proteins on patched signalling) constructs in both human and animal subjects. A bioactive polypeptide comprising amino acids 28-202 of human Ihh is preferred. The products can also be used for the maintenance of differentiated concurred the constructs arising from the use of ceretal of treat the constructs.
                                                                                                                                              neuronal cells in an animal. They can be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the prevention and/or treatment of hypoxia, e.g. as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ONTO-) ONTOGENY INC. Mahanthappa NK, Miao N, Pang K, Wang M; WPI; 99-142578/12.
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24-JUL-1997; US-900220.
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    PT A new method to regulate muscle growth
PS Disclosure; Page 120-121; 130pp; English.
PS Disclosure; Page 120-121; 130pp; English.
PS Disclosure; Page 120-121; 130pp; English.
CC The present sequence is human Indian hedgehog protein Ihh. The
CC invention relates to a method for modulating the formation and/or
CC cells, especially muscle tissue by ecotopically contacting muscle
CC cells, especially muscle stem/progenitor cells, in vitro or in
CC vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and
CC enclosure that mimics the effect of hedgehog polypeptides and
CC signalling, or activates or potentiates patched signalling) in an
CC amount effective to alter the growth state of the treated cells.
CC of, or surgical or cosmetic repair of, such muscle tissues, by
CC official and bedgehog polypeptide or ptc therapeutic. The
CC disorder may be muscle atrophy, in particular skeletal muscle
CC atrophy or cardiac muscle atrophy, cachaxia, or muscular myopathy
CC (all calimed). The hedgehog polypeptide or ptc therapeutic can
CC inhibit growth of myoblastic drained). The hedgehog therapeutic
CC myoblastic or neoplastic growth of muscle tissue such as in
CC myoblastic sarcoma (also claimed). The hedgehog therapeutic
CC preferably comprises at least a bloactive extracellular portion of
CC an hedgehog protein (see Y05510-19) encoded by a vertebrate hedgehog
CC gene (see X2598-107), especially a human hedgehog gene.

Sequence 411 Aa:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hughes SM, Ingham
WPI; 99-243557/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Indian hedgehog protein Ihh.
Indian hedgehog; Ihh protein; human; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atro
cachexia; muscular myopathy; myoblastic sarcoma; therapy.
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29-AUG-1997; US-057394.
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Query Match Best Local Similarity

100.0%; ilarity 100.0%; Conservative

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Mismatches

Indels Length

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Gaps

0

411;

Score 2175; Pred. No. 1

Matches

411;

Gaps

0

60

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PT Method for limiting damage to neurons caused by ischaemic or epoxic productions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks Disclosure; Page 66-68; 104pp; English.

CC A method has been developed for limiting the damage to neuronal cells by construct provide a provide and transient or epoxic conditions by administering a ptc (patched) construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct station of the ptc therapeutic agent is used to protect construct station of the ptc therapeutic agent is used to protect construct tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic consephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The creatment reduces CIV by at least 25, particularly at least 70,%. The present sequence represents a hedgehog sequence given in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell brain infarction; cerebral infarction; transient ischaemic attack; stroke; cerebral infarct volume, spinal cord; oedema; trauma; haemorrhage; encephalomyelitis; coronary bypass; cerebral hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse Ihh hedgehog protein sequence. Patched; hedgehog; ptc therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W94470 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mahanthappa NK;
WPI; 99-095458/08.
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27-JUN-1997; US-883656
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PT Increasing the survival of neuronal, dopaminergic and GABA-nergic processing the survival of neuronal, dopaminergic and GABA-nergic processing the survival derived from hedgehog polypeptides, useful in the treatment of parkinson's disease.

PT Increasing the parkinson's disease pisculation is based on the finding that hedgehog protein. The CC ratis polypeptide is mouse inh Indian hedgehog proteins are useful convention is based on the finding that hedgehog proteins are useful convention is based on the finding that hedgehog proteins are useful convention is based on the finding that hedgehog proteins of convences protective agents in the treatment and prophylaxis of convence compared in the loss of tissue from the cand/or GABA-nergic neurons, or the general loss of tissue from the construct of GABA-nergic neurons, or the general loss of tissue from the cand/or GABA-nergic neurons, or the general loss of tissue from the cand-or GABA-nergic neurons, or the general loss of tissue from the cand-or GABA-nergic neurons, or the general loss of tissue from the cand-or GABA-nergic neurons, or the general loss of tissue from the cand-or GABA-nergic neurons, or the general loss of tissue from the cand-or GABA-nergic neurons, or the general loss of tissue from the cand-or GABA-nergic neurons, or the general loss of tissue from the cand-or GABA-nergic neurons or the general loss of tissue from the cand-or GABA-nergic neurons or the general loss of tissue from the cand-or GABA-nergic neurons or the general loss of tissue from the cand-or GABA-nergic neurons or the general loss of tissue from the cand-or GABA-nergic neurons or the general loss of tissue from the cand-or GABA-nergic neurons or the general loss of tissue from the cand-or GABA-nergic neurons or the general loss of tissue from the general l
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24-JUL-1998;
24-JUL-1997;
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W97767;
21-MAY-1999
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Mahanthappa NK, Miao N, Pang
WPI; 99-142578/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Indian hedgehog (Ihh) protein.
Indian hedgehog; Ihh protein; mouse; dopaminergic; GABA-ner
ptc therapeutic; patched; signal transduction; Parkinson's
Huntington's disease; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; X07273.
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Pred. No. 5.3e-200;
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Best Local
Matches 38
                                                                                                                                                                                                                                                                                                                             04-MAR-1999.
28-AUG-1998; U17922.
29-AUG-1997; US-057394.
(ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hughes SM, I
WPI; 99-243557/20.
N-PSDB; X25100.
A new method to regulate muscle growth Disclosure; Page 114-115; 130pp; English.
The present sequence is mouse Indian hedgehog protein Ihh. The invention relates to a method for modulating the formation and/or maintenance of muscle tissue by ecotopically contacting muscle cells, especially muscle stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and gene therapy constructs) or put therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the growth state of the treated cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-1999 (first entry)
Mouse Indian hedgehog protein Ihh.
Indian hedgehog; Ihh protein; mouse; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy.
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RR7350LT
RR7
therapy.

Claim 17; Page 137-38; 210pp; English.

The sequence represents a mouse Indian
to a Drosophila hedgehog protein (R773
                                                                                                                                                                           Ingham PW, Mcmahon AP, Tabin CJ;
WPI; 95-255060/33.
N-PSDB; 091640.
Hedgehog-like protein(s) and nucleic acid(s) encoding to treat degenerative nervous system disorder(s) and j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1994; U14992.
30-DEC-1993; US-176427
14-DEC-1994; US-356060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; Indian hedgehog protein; probe; nervous system disorder; gene therapy;
                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE.
(IMCR ) IMPERIAL CANCER
Ingham PW, Mcmahon AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse Indian
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bin CJ;
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antibody.
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Indian hedgehog protein, (R77337), and is encoded

encoded

homologous d by a cDNA

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Best Loc
Matches
                                                                                                                                                                                                 30-DEC-1994; U14992.
30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
(HARD ) HARVARD COLLEGE.
(IMCR ) IMPERIAL CANCER RE
Ingham PW, Mcmahon AP, 17
WPI; 95-255060/33.
N-PSDB; 091641.
                   Claim 17; Page 146-47; 210pp; English.

Claim 17; Page 146-47; 210pp; English.

The sequence represents a mouse Indian hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and is encoded by a cDNA isolated by screening of a human fetal lung 5'-stretch plus cDNA library. Probes and primers derived from hedgehog sequences may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene antibodies generated from the protein may be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated by low stringency screening of a mouse genome DNA library and screening of an 8.5 day post coitum cDNA library. Probes and primers derived from hedgehog sequences may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the protein may be used as therapeutic or research reagents.
                                                                                                                                                                    Hedgehog-like protein(s) and nucleic acid(s) encoding them to treat degenerative nervous system disorder(s) and in gene
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
WO9518856-A1.
                                                                                                                                                                                                                                                                                                                                                                            Human; Indian hedgehog protein; probe; nervous system disorder; gene therapy;
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Human; Indian hedgehog proteir
                therapeutic
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30-DEC-1994;
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hes 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPGEGVHWYPQLLYRLGRLLLEEGSFHPLGMSGAGS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVAAVSTHVALGAYAPLIKKGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFHSLAWGSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFQVIETQDPPRRLALTPAHLLFIADNHTEPAAHFRATFASHVQPGQYVLVSGVPGLQPA
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 312 AA;
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Pred. No. 6.6e-164;
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            program (s)

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07-0CT-1997; U15753.
02-0CT-1997; US-061323.
07-0CT-1996; US-729743.
(UYJO) UNIV JOHNS HOPKINS S
Beachy PA, Porter JA;
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20-OCT-1998 (first entry)
20-OCT-1998 (first entry)
Mouse sonic hedgehog (shh) protein.
Mouse sonic hedgehog in euronal cell proliferation; zebrafish; shh;
Cholesterol biosynthesis; pituitary gland gene expression; mouse;
Cholesterol biosynthesis; pituitary gland gene expression; mouse;
tiggy-winkle hedgehog protein; twhh; sonic hedgehog; major limb tr:
tiggy-winkle hedgehog protein; twhh; sonic hedgehog; major limb tr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 98-399053/24.

New hedgehog-derived poly:peptide(s) - used to develop products modulating proliferation or differentiation of neuronal cells, cholesterol biosynthesis or transport or expression of pituitary
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                                                                                                                                   30-DEC-1994; U14992.
30-DEC-1993; US-376427.
14-DEC-1994; US-356060.
(HARD) HARVARD COLLEGE.
(IMCR) IMPERIAL CANCER RES TECH
Ingham PW, Mcmahon AP, Tabin C
The sequence represents a mouse sonic hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and is encoded by a cDNA isolated from an 8.5-day post coitum mouse clibrary. Probes and primers derived from the sonic hedgehog cmay be used as diagnostic agents for neuromuscular, autonomic
                                                             Claim
                                                                                                          WPI; 95-255060/33.
N-PSDB; Q91637.
                                                                                                                                                                                                                                                                                                                                 08-MAR-1996 (first entry)
Mouse sonic hedgehog protein.
Mouse; sonic hedgehog protein;
nervous system disorder; gene t
                                                                                    Hedgehog-like protein(s)
to treat degenerative nea
                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                           R77339 standard; Protein; 437
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                                                             17; Page 139-41; 210pp; English.
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                                                                                                                                                                                                                                               /note=
279
                                                                                                                                                                                                                                                                       /note=
25. .30
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                     nervous
                                                                                                                                                                                                                                 "N-linked glycosylation
                                                                                                                                                                                                                                                           "conserved sequence (R77349)"
                                                                                                                                                                                                                                                                                "signal peptide
                                                                                   and nucleic rvous system
                                                                                                                                                                                                                                                                                                                                 otein; probe; primer; diagnostic;
gene therapy; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                               TECHNOLOGY.
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Pred. No. 3e-122;
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                                                                                  acid(s) encoding
disorder(s) and disorder
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425
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ETMHPLGMA
                     GSFHPLGMS
                                                                      LRLFHSL----
                                                                                                            VPG----LQPARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWP
                                                                                                                                                            EPHRLRAFQVIETODPPRRLALTPAHLLFTA-DNHTEPAARFRATFASHVQPGQYVLVAG
                                                                                                                                                                                         VKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDR
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                                              FRLAHALLAALAPARTDGGGGGSIPAAQSATEARGA-EPTAGIHWYSQLLYHIGTWLLDS
                                                                                            ERGGDRRLLPAAVHSVTLREEEAGAYAPLTAHGTILINRVLASCYAVIEEHSWAHRAFAP
                                                                                                                                           DEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGPSALFASRVRPGQRVYVVA
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                                                                                                                                                                                                                                                                                                                                                                                             261;
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                     407
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 1276.5; DE Pred. No. 6e-122;
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RESULT
W94471
07-JAN-1999.
26-JUN-1998;
27-JUN-1997;
                                                                                                                                                                                                                                                                           Mouse Shh hedgehog protein sequence.

Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal brain infarction; cerebral infarction; transient ischaemic att stroke; cerebral infarct volume; spinal cord; oedema; trauma; haemorrhage; encephalomyelitis; coronary bypass; cerebral hypo
                                                                                                                                                                            Mahanthappa NK;
WPI; 99-095458/08.
                                                                                                                                                                                                                                                                                                                                                              W94471 standard; Protein; W94471;
                                                                                                                                                                                                    (ONTO-) ONTOGENY INC
                                                                                                                                                                                                                                                         WO9900117-A2.
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US-883656.
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W97768
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Best Local Similarity
Matches 261; Conserv
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N-PSDB; X07274.
Increasing the survival of neuronal, dopaminergic and GABA-cells - by using a ptc therapeutic such as a protein kinass thibitor, or an agent derived from hedgehog polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Sonic hedgehog (Shh) protein.
Sonic hedgehog; Shh protein; mouse; dopaminergic; GABA-nergic;
ptc therapeutic; patched; signal transduction; Parkinson's dis
Huntington's disease; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                        04-FEB-1999.
24-JUL-1998; U15419.
24-JUL-1997; US-900220.
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                                                                                                                                                        WPI; 99-142578/12.
                                                                                                                                                                                    (ONTO-) ONTOGENY INC.
Mahanthappa NK, Miao N, Pang
                                                                                                                                                                                                                                                                                                                                                               WO9904775-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  cerebral ischaemia;
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; Pred. No. 6e-122;
40; Mismatches 91;
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                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective;
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uch as a protein kinase
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                        useful
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   OK KWE DAC
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Disclosure; Page 89-91; 138pp; English.
This polypeptide is mouse shh Sonic hedgehog protein. The
invention is based on the finding that hedgehog proteins are useful
as protective agents in the treatment and prophylaxis of
neurodegenerative disorders resulting from the loss of dopaminergic
and/or GABA-rergic neurons, or the general loss of tissue from the
substantia nigra. Exemplary disorders include Parkinson's disease,
Huntington's disease (both claimed), amyotrophic lateral sclerosis
and cerebral ischaemia. The invention relates to hedgehog
therapeutics (i.e. hedgehog polypeptides and gene therapy constructs
e.g. constructs encoding recombinant hedgehog gone therapy constructs
trans-activation constructs for altering hedgehog gene regulatory
sequences) and ptc therapeutics (i.e. agents which mimic the effect
of naturally occurring hedgehog proteins on patched signalling)
that are effective in both human and animal subjects. Human lih
and Dhh polypeptides (see w97763-64) are preferred. The products
can also be used for the maintenance of differentiated neurons in
cultures, and to enhance the implantation of such neuronal cells in
an animal. They can be used to prevent or treat neurodegenerative
conditions arising from the use of certain drugs, and ip the
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Best Local S
Matches 261
               Mouse Sonic hedgehog protein Shh. sonic hedgehog; Shh protein; mouse; hedgehog; Shh protein; mouse; hedgehog therapeutic; ptc therapeutic; patched; signal transduction; muscle atracachexia; muscular myopathy; myoblastic sarcoma; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevention and/or treatment of hypoxia, e.g. as a neuroprotective agent.
                                                                                              05-JUL-1999
                                                                                                              Y05513;
                                                                                                                              Y05513 standard; Protein; 437
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nes 261; Conserv
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                                                                                             (first entry)
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                                   muscle atrophy;
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PS Disclosure; Page 115-116; 130pp; English.

CC The present sequence is mouse Sonic hedgehog protein Shh. The

CC invention relates to a method for modulating the formation and/or

CC cells, especially muscle stem/progenitor cells, in vitro or in

CC vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and

CC gene therapy constructs) or ptc therapeutic (i.e. a small organic

CC molecule that mimics the effect of hedgehog proteins on patched

CC signalling, or activates or potentiates patched signalling) in an

CC amount effective to alter the growth state of the treated cells.

CC of, or surgical or cosmetic repair of, such muscle tissues, by

CC administering a hedgehog polypeptide or ptc therapeutic. The

CC altrophy or cardiac muscle atrophy, in particular skeletal muscle

CC altrophy or cardiac muscle atrophy, cachaxia, or muscular myopathy

CC altrophy or cardiac muscle atrophy, cachaxia, or muscular myopathy

CC altrophy or cardiac muscle atrophy, cachaxia, or muscular myopathy

CC altrophy or cardiac muscle atrophy, cachaxia, or muscular myopathy

CC altrophy or cardiac muscle atrophy, cachaxia, or muscular myopathy

CC altrophy or cardiac muscle atrophy cachaxia, or muscular myopathy

CC altrophy or cardiac muscle atrophy cachaxia, or muscular myopathy

CC altrophy or cardiac muscle atrophy cachaxia, or muscular myopathy

CC altrophy or cardiac muscle atrophy therapeutic can

CC myoblastic sarcoma (also claimed). The hedgehog therapeutic

CC myoblastic sarcoma (also claimed). The hedgehog therapeutic

CC myoblastic sarcoma (also claimed). The hedgehog such as in

CC myoblastic sarcoma (also claimed). The hedgehog such as in

CC myoblastic sarcoma (also claimed). The hedgehog such as in

CC myoblastic sarcoma (also claimed). The hedgehog hadden per can be degehog ene (see x25098-107), especially a human hedgehog gene.
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Bladgen CS, Currie PD, Hughes SM, Ingham
WPI; 99-243557/20.
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04-MAR-1999.
28-AUG-1998; U17922.
29-AUG-1997; US-057394.
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ETMHPLGMA
                                          GSFHPLGMS 407
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                                                                                    FRLAHALLAALAPARTDGGGGGSIPAAQSATEARGA-EPTAGIHWYSQLLYHIGTWLLDS
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Pred. No. 6e-122;
0; Mismatches 91;
                                                                                                                -----AWGSWTPGEGVHWYPQLLYRLGRLLLEE 398
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PS Claim 13: Pages 150-151; 210pp; English.

CC This represents a zebrafish sonic hedgehog (shh) protein sequence. The CC invention provides methods and compounds for modulating proliferation or CC differentiation of neuronal cells, cholesterol biosynthesis or transport in a cell comprises contacting a CC cholesterol biosynthesis or transport in a cell comprises contacting a CC cell with a compound that affects hedgehog, thereby affecting cholesterol biosynthesis or transport. The methods for inhibiting the neural inducing a CC cell with a compound that affects hedgehog, thereby affecting cholesterol biosynthesis or transport. The methods for inhibiting the neural inducing a critvity of a hedgehog polypeptide in cells, and for inducing pituitary CC gland gene expression utilises sequences selected from a zebrafish cc tiggy-winkle hedgehog (twhh) protein (W61487) or a mouse shh cc tiggy-winkle hedgehog (twhh) protein (W61487) or a mouse shh cc protein (W61488). The products and methods provide for compounds which can affect hedgehog activity. They can be used for treating disorders which arise from neuronal degeneration or abnormal function. They can calso be used for treating smith-Lemli-Optiz syndrome. The products can so be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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17-OCT-1997; U15753.

02-OCT-1997; U15761323.

02-OCT-1996; US-061323.

07-OCT-1996; US-729743.

(UYJO) UNIV JOHNS HOPKINS SCHOOL OF MEDICINE.

Beachy PA, Porter JA;

WPI; 98-399053/34.

New hedgehog-derived poly:peptide(s) - used to develop products for modulating proliferation or differentiation of neuronal cells, cholesterol biosynthesis or transport or expression of pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zebrafish sonic hedgehog (shh) protein.
Hedgehog polypeptide; neuronal cell proliferation; zebrafish;
Cholesterol biosynthesis; pituitary gland gene expression; shh;
tiggy-winkle hedgehog protein; twhh; sonic hedgehog; major limb trauma;
neuronal degeneration; nerve-sparing agent; Smith-Lemil-Optiz syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W61486 standard; Protein; 418
W61486;
20-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9830576-A1.
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364 LRLFH---
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                                                                                                                                                                                                                                                                                 VKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRYEGKIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLRPRLHFCLVLLLLLVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGAS
                                                                                                                                     LVAGVPG-LQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCEAAVADHHLAQLAFWP
                                                                                                                                                                                                                                                                                                                                                                                                                       HVHCSVKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVL
                                                                                                    MVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTIVVDRILASCYAVIEDQGLAHLAFAP
                                                                                                                                                                                                                                                                                                                                                                                   HIHCSVKAENSVAAKSGGCFPGSALVSLQDGGQKAVKDLNPGDKVLAADSAGNLVFSDFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKLRVTEGWDEDGHHFEESLHYEGRAVDITTSDRDKSKYGTLSRLAVEAGFDWVYYESKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMNHWPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLLTRVLLVSLLTLSLVV-SGLACGPGRGYG-RRRHPKKLTPLAYKQFIPNVAEKTLGAS
                                                                                                                                                                                                                                          MFTDRDSTTRRVFYVIETQEPVEKITLTAAHLLFVLDNSTEDLHTMTAAYASSVRAGQKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.6%;
                                SLAWGSWTPGEGVHWYPQLLYRLGRLLLEEGSFHPLGMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1274; DB 1;
Pred. No. le-121;
6; Mismatches 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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Best Local Similarity
Matches 267; Conserv
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30-DEC-1994; U14992.
30-DEC-1994; US-176427.
14-DEC-1994; US-356060.
(HARD ) HARVARD COLLEGE.
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
Ingham PW, Mcmahon AP, Tabin CJ;
WPI; 95-25506/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapy.

Claim 17; Page 143-45; 210pp; English.

The sequence represents a human sonic hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and is encoded by a cDNA isolated from a human fetal lung cDNA library. Probes and primers derived from the sonic hedgehog gene may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy.

Antibodies generated from the protein may be used as therapeutic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q91639.
Hedgehog-like protein(s) and nucleic acid(s) encoding them -
to treat degenerative nervous system disorder(s) and in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human sonic hedgehog protein.
Human; sonic hedgehog protein; probe; primer; diagnostic;
nervous system disorder; gene therapy; antibody.
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                research reagents.
Sequence 475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9518856-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 ARLYYYVSSFLFPQNSSSRSNATLQQEGVHWYSRLLYQMGTWLLDSNMLHPLGMS 414
366
                           350
                                                         306
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                                                                                                                                                                          CLLLVLVSSLLVCSGLACGPGRGFG-KRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEGK
                                                                                                                                                                                                                                                                                                                                                                             CLVLLLL--LVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGK 70
VIEEHSWAHRAFAPFRLAHALLAALAPARTDRGGDSGGGDRGGGGGRVALTAPGAADAPG
                                                                                                                                PHRLRAFQVIETQDPPRRLALTPAHLLFTA---DNHT-EPAARF------RATF 294
                                                                                                                                                                                                                                                     EGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSV
                                                                                                                                                                                                                                                                                                                  IARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWBGVKLRVT 130
                           AVADHHLAQLAFWPLRLFHSL-----
                                                       ASHVQPGQYVLVA----GVPGLQPARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFA 349
                                                                                                                    DGAKKVFYVIETREPBERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALF
                                                                                                                                                                                                                                         EGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSV
                                                                                                                                                                                                                                                                                                  ISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVT
                                                                                                                                                                                                                                                                                                                                                                                                                     58.4%; score 1271; DB 1; ilarity 57.7%; Pred. No. 2.5e-121; Conservative 45; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "unspecified amino acid"
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                             ----AWGSWTPG
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----EGVHWYPQLLYRLGRLLLEEGSFHPLGMS------GAG
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AGATAGIHWYSQLLYQIGTWLLDSEALHPLGMAVKSSXSRGAG
    468
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Search completed: June Job time: 2583 sec Ç 2000, 08:16:18

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Minimum
Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
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Listing first 45 summaries
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     score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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1246.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is the number of results predicted by chance to have a ater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
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     US-08-900-220-16
2175
1 MSPARLRPRLHFCLV
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/5COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/backfiles1.pep:*
     2000, 07:55:36; Search time 45.88 Seconds
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129.332 Million cell updates/sec
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US-08-176-427B-6
US-08-356-060A-10
US-08-356-060A-10
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PCT-US95-15923-20
US-08-356-060A-11
PCT-US95-15463-18
US-08-356-060A-13
US-08-356-060A-13
US-08-356-060A-8
US-08-356-060A-8
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                              Sequence 6, Appli Sequence 11, Appl Sequence 20, Appl Sequence 21, Appl Sequence 11, Appl Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 19, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 19, Appli Sequence 31, Appli 
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
128	139	145	147	164	167	263	263	300.5	300.5	314	314	315	315	346	346
5.9	6.4	6.7	6. 8	7.5	7.7	12.1	12.1	13.8	13.8	14.4	14.4	14.5	14.5	15.9	15.9
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US-08-748-591-6	US-08-748-591-7	US-08-748-591-8	US-08-748-591-1	US-08-748-591-2	US-08-748-591-3	US-08-356-060A-37	US-08-176-427B-14	US-08-356-060A-16	US-08-176-427B-16	US-08-356-060A-17	US-08-176-427B-17	US-08-356-060A-15	US-08-176-427B-15	US-08-356-060A-35	US-08-176-427B-12
Sequence 6, Appli	Sequence 7, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 37, Appl	•	•	Sequence 16, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 15, Appl	`	Sequence 35, Appl	•

ALIGNMENTS

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SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-176-427B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 6, Application; Patent No. 5789543; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-176-427B-6
                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATTHEW P.
REGISTRATION UNDMER: HMI-006
REFERENCE/DOCKET NUMBER: HMI-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-740
TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NO: 6:
SECTIONE CHARACTERS TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 60 St
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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136 DGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHS 195

76 ERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDE 135

9; Mismatches Score 1686; DB 1; Pred. No. 2.1e-168; 9; Mismatches 8;

Length 336; Indels

0;

0

ERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGRDE 60

pest Local Similarity 94.9%; Matches 319; Conservative

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RESULT 2
US-08-356-060A-10
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                                                                                                                                    US-08-356-060A-10
                                                          Query Match
Best Local Similarity
Matches 319; Conserv
                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, METCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 227-7400
TELEPAX: (617) 227-7591
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION MOMBER: US/08/356,060
FILING DATE: 14-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALUXXX
STREET: UC
CITY: BOSTON
STATE: MA
COUNTRY: USA
COUNTRY: USA
COUNTRY: OSADA
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                       TYPE: amino acid
                             76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFHSLAWGSW 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ), Application US/08356060A
5844079
                                                                                                                                                                                          336 amino acids
                                                            Conservative
                                                                                                                                                                 linear
                                                                                                                                               protein
                                                                      77.5%;
94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/356,060A
                                                                        Score 1686; DB 2;
Pred. No. 2.1e-168;
                                                                                                                                                                                                                                                                                   HMI-006CP
                                                          9; Mismatches
                                                                                      Length 336;
                                                         Indels
                                                         0;
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101 RLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDR 160

0

Gaps

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RESULT 3
US-08-356-060A-14
; Sequence 14, Application US/08356060A
; Patent No. 5844079
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                                                                                                                                                NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-9941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
TOPDICGY: 11004T
  Query Match
Best Local Similarity
Matches 311; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427
APPLICATION NUMBER: US/08/176,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 RVAAVSTHVALGSYAPLTRHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFPSLAWGSW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 RVAAVSTHVALGAYAPLIKHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFHSLAWGSW 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AFQVIETQDPPRRLALTPAHLLFIADNHTEPAAHFRATFASHVQPGQYVLVSGVPGLQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 AFQVIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQPGQYVLVAGVPGLQPA 315
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ZIP: 02109
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75.7%; Score 1646; DB 2; ilarity 100.0%; Pred. No. 2.8e-164; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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14-DEC-1994
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                                    Length 313;
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PCT-US95-15463-20
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GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
                                                                                                            Best Local Similarity
Matches 262; Conserv
                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                   TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 DNHTEPAARFRATFASHVQPGQYVLVAGVPGLQPARVAAVSTHVALGAYAPLTKHGTLVV
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STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                70 KIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRV 129
                                                                 13 CLVLLL----LLVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEG 69
                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/15463 FILING DATE: 01-DEC-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 92037
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                                                                                                                                                                                                                                                                                                                    ELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAVRPGDRVLAMGEDGSPTFSDVLIFLDREPHRLRAFQVIETQDPPRRLALTPAHLLFTA 280
                                               FHPLGMSGAGS 411
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                                                                                                                                                                                                                                                     437 amino acids
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                                                                                                              Conservative
                                                                                                                         58.8%;
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                                                                                                            39; Mismatches
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                                                                                                         Score 1279.5; DB 4;
Pred. No. 1.2e-125;
39: Mismatches 91;
                                                                                                            Indels 37;
                                                                                                                                            Length 437;
                                                                                                            Gaps
                                                 65
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13 CLVLLL----LLVVPAAMGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEG 69

Indels

37;

Gaps

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CFLVILASSLLVCPGL-ACGPGRGFG-KRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEG

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                                                                                                ; TOPOLOGY: 11; MOLECULE TYPE: PCT-US95-15923-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application PC/TUS9515923
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine,
ITILE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
Query Match 58.8
Best Local Similarity 61.1
Matches 262; Conservative
                                                                                                                                                                                                                   TELEPHONE: 619/678-50
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Haile, Lisa A. REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 TEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWYYYESKAHVHCS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 VPG----LQPARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWP 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 VKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 ETMHPLGMA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 ERGGDRRLLPAAVHSVTLREEEAGAYAPLTAHGTILINRVLASCYAVIEEHSWAHRAFAP 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 DEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGPSALFASRVRPGQRVYVVA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 EPHRLRAFQVIETQDPPRRLALTPAHLLFTA-DNHTEPAARFRATFASHVQPGQYVLVAG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 VKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLTFLDR 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 GSFHPLGMS 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92037
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: CA
                                                                                                                                                         amino acid
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58.8%; Score 1279.5; DB 4; 61.1%; Pred. No. 1.2e-125; vative 39; Mismatches 91;
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                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATTHEW 36,709
REGISTRATION NUMBER: 4MI-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1077400
                                                       TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,4:
FILING DATE: 30-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.
TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 33
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N: 435
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Best Local Similarity
               APPLICATION NUMBER: US 08/176,427
ETILING DATE: 30-DEC-1993
ATTORNEY_AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                               APPLICATION NUMBER: US/08/356,060A FILING DATE: 14-DEC-1994 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION DATA:
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(617) 227-7400
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Pred. No. 2.4e-125;
Pred. No. 2.4e-125;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-356-060A-11
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PCT-US95-15463-18
                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application PC/TUS9515463
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 20
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Best Local Similarity
Matches 261; Conservat
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15463
FILING DATE: 01-DEC-1995
                                                                                                                        COMPUTER READABLE FORM:
MEDIIM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 92037
                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSFHPLGMS 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETMHPLGMA 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHRLRAFQVIETQDPPRRLALTPAHLLETA-DNHTEPAARFRATFASHVQPGQYVLVAG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDR 249
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                                                                                                                                                                                                                                                       : La Jolla
E: CA
                                                                                                                                                                                                                                                                                          E: Fish & Richardson P.C. 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.7%; Score 1276.5; DB·2; illarity 60.8%; Pred. No. 2.4e-125; Conservative 40; Mismatches 91;
 38,347
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GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine,
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.6%; Score 1274; DB 4; Best Local Similarity 61.2%; Pred. No. 4.1e-125;
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TELEFAX: 619/678-5099
TRECERNATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
                                                                                                                                                                                                                                                                                                            ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                              CLASSIFT O A CLASS
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4225 L. CITY: La Jolla
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07265/043WO1
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TELECOMMUNICATION INFORMATION:

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RESULT 10
US-08-356-060A-13
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: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US95-15923-18
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Best Local Similarity 61.2%;
Matches 254; Conservative 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
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TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                       CITY: Boston
STATE: MA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVAGVPG-LQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWP 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MFTDRDSTTRRVFYVIETQEPVEKITLTAAHLLFVLDNSTEDLHTMTAAYASSVRAGQKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLLTRVLLVSLLTLSLVV-SGLACGPGRGYG-RRRHPKKLTPLAYKQFIPNVAEKTLGAS 59
                                                                                                                                                                                            02109
                                                                                                                                                                                                                                                                              60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SLAWGSWTPGEGVHWYPQLLYRLGRLLLEEGSFHPLGMS 407
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Matches
                                                                           Sequence 2, Application US/08176427B Patent No. 5789543
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ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
NAME: Vincent, Matthew P.
NAME: Vincent, Matthew P.
NAME: Vincent, Matthew P.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.
                                                                                                                                                                                          306 ASRVRPGQRVYVVAERDGDRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLASCYA
                                                                                                                                                                                                                                                                                                                                                                                       295
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                                                                                                                                                                                                                                                                      366 VIEEHSWAHRAFAPFRLAHALLAALAPARTDRGGDSGGGDRGGGGGRVALTAPGAADAPG
                                                                                                                                                                                                                                                                                                          13 CLVLLLL--LVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGK 70
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nes 267; Conserv
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                                                                                                                                                                                                                                                                                                                                                                   ASHVQPGQYVLVA----GVPGLQPARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFA 349
                                                                                                                                                                                                                                                                                                                                                                                                                         DGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDRD 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSV 185
                                     Ingham, Phillip W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.4%; Score 1271; DB 2; Length 475; 57.7%; Pred. No. 1e-124; ative 45; Mismatches 85; Indels 6
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TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS:

STREET: CITY: E

60 State Street

LAHIVE & COCKFIELD

ADDRESSEE:

STATE:

: Boston E: MA TRY: USA

COUNTRY: U ZIP: 02109

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

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US-08-356-060A-8
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                                                                GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.

APPLICANT: MICHAION, Andrew P.

APPLICANT: Tabin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08, FILING DATE: 30-DEC-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Vincent, Matthew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 227-7400
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CURRENT APPLICATION DATA:
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
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                                                                                                                                                                                                                                                                                                                                                                                    378
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 LVVPAAMGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGKIARSSERFK 79
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REFERENCE/DOCKET NUMBER: HMI-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAK 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IETQDPPRRLALTPAHLLFTADNHTEPAA----RFRATFASHVQPGQYVLVAGVPGLQ-- 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PASVHSVSLREEASGAYAPLTAQGTILINRVLASCYAVIEEHSWAHWAFAPFRLAQGLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYSDFLTFLDRMDSSRKLFYV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IETROPRARLLLTAAHLLFVAPQHNQSEATGSTSGQALFASNVKPGQRVYVLGEGGQQLL 317
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60 State Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/176,427B
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                                                           US-08-748-591-4; Sequence 4, Application US/08748591; Patent No. 5759811; GENERAL INFORMATION:
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APPLICANT:
APPLICANT:

APPLICANT: Epstein, Ervin APPLICANT: Hu, Zhilan APPLICANT: Bonifas, Jeanette TITLE OF INVENTION: Mutant Human Hedgehog Gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: HMI-006CP TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,01
FILING DATE: 14-DEC-1994
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                  314 PARVAAVS-THVALGAYAPLIKHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFHSLAW 372
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378 ALCPDGAIPTAATTTTGIHWYSRLLYRIGSWVLDGDALHPLGMVAPAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Vincent, Matthew P
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                         G-----SWTPGEGVHWYPQLLYRLGRLLLEEGSFHPLGMSGAGS
                                                                                PASVHSVSLREEASGAYAPLTAQGTILINRVLASCYAVIEEHSWAHWAFAPFRLAQGLLA
                                                                                                                                                                                                                                                                                           TGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREPHRLRAFQV 259
                                                                                                                                                                                                                                                                                                                                                   SEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHSAAAK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                      ELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHH 139
                                                                                                                                                                IETRQPRARLLLTAAHLLFVAPQHNQSEATGSTSGQALFASNVKPGQRVYVLGEGGQQLL
                                                                                                                                                                                                                                              SGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYSDFLTFLDRMDSSRKLFYV
                                                                                                                                                                                                                                                                                                                                    SEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWYYYESKAHIHCSVKAENSVAAK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLVSSGLTCGPGRGIG-KRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEGKITRNSERFK 77
                                                                                                                                                                                                       IETQDPPRRLALTPAHLLFTADNHTEPAA----RFRATFASHVQPGQYVLVAGVPGLQ--
                                                                                                                                                                                                                                                                                                                                                                                                                    ELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEDGHH 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 425 amino acids amino acid
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Gaps

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NUMBER OF SEQUENCES:

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RESULT 14
US-08-748-591-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 854-0875 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 EGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWYYYESKAHVHCSV 190
                                                                                                                                                                                                                                                                                              246
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                                                                          426 AGATAGIHWYSQLLYQIGTWLLDSEALHPLGMA 458
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                                                                                                                                                                                  251 PHRLRAFQVIETQDPPRRLALTPAHLLFTA---DNHT-EPAARF------RATF 294
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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APPLICANT: Epstei
APPLICANT: Hu, Zh
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TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Mutant Human Hedgehog Gene
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                            350 AVADHHLAQLAFWPLRLFHSL-----
                                                                                                                                                                                                                                                                                                        126 EGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSV
                                                                                                                                                                                                                                                                                                                            131 EGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWYYYESKAHVHCSV 190
366 VIEEHSWAHRAFAPFRLAHALLAALAPARTDRGGDSGGGDRGGGGGRVALTAPGAADAPG
                                                                                                                295 ASHVQPGQYVLVA----GVPGLQPARVAAVS-THVALGAYAPLTKHGTLVVEDVVASCFA 349
                                                                                                                                                   246 DGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGPPSGGALGPRALF
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CITY: Menlo Park
STATE: CA
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                                                                          ASRVRPGQRVYVVAERDGDRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILINRVLASCYA
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PCT-US95-02315-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             Query Match 57.3%; Score 1246.5; DB 4; Best Local Similarity 59.9%; Pred. No. 3.3e-122; Matches 257; Conservative 40; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: John P. White
REGISTRATION UNMER: 28,678
REFERENCE/DOCKET NUMBER: 4537
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US95/02315
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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246 DEGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSGPTPGPSPLFASRVRPGQRVYVVA 305
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                        EPHRLRAFQVIETQDPPRRLALTPAHLLFTA-DNHTEPAARFRATFASHVQPGQYVLVAG 308
                                                                                                        VKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDR 249
                                                                                                                                                                                                                 KITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRV 125
                                                                       VKAENSVAAKSDGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTFLDR 245
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Edlund, Thomas
Edlund, DA ENCODING A VERTEBRATE HOMOLOG OF
NVENTION: LABGEHOG, VHH-1, EXPRESSED BY THE NOTOCHORD, AND USES
NVENTION: THEREOF
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                                                                                                                              ERGGDRRLLPAAVHSVTLREEAAGAYAPLTADGTILINRVLASCYAVIEEHSWAHRAFAP
                                                              FRIAHALLAALAPARTDGGGGGSIPAPQSVAEARGAGPPA-GIHWYSQLLYHIGTWLLDS
                                                                                  -----AWGSWTPGEGVHWYPQLLYRLGRLLLEE 398
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RESULT 2'
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Sonic hedgehog protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C:Accession: A49425
R;Echelard, Y.; Epstein, D.J.; St-Jacques. R . Shon T . Maillen.
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(;Species: Mus musculus (house mouse)
(;Species: Mus musculus (house mouse)
(;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
(;Accession: C49425
R;Echelard, Y:; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; M
(cell 75, 1417-1430, 1993
A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is imp
A;Recession: C49425
A;Accession: C49425
A;Accession: C49425
A;Status: preliminary
A;Status: preliminary
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A; Residues: 1-336 <ECH>
A; Cross-references: GB: X76291
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RESULT 8
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Besert hedgehog protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
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A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is A; Reference number: A49425; MUID:94094334
A; Recession: B49425
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A;Molecule type: DNA
A;Residues: 1-396 <ECH>
A;Cross-references: GB:X76292;
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                                                                                      PVLLFLDRDLQRRASFVAVETERPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1175; DB 2;
pred. No. 5.5e-92;
50; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:CAA53924.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID:g443942
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C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
C;Accession: A46400; JW0501; A43480
Genes Dev. 6, 2635-2645, 1992
A;Title: The Drosophila hedgehog gene is expressed specifically in posterior A;Reference number: A46400; MUID:94040725
A;Raccession: A46400
A;Raccession: A46400
A;Status: Nov-1992
A;Title: The Drosophila hedgehog gene is expressed specifically in posterior A;Reference number: A46400; MUID:94040725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-471 <TAS>
A; Residues: 1-471 <TAS>
A; Residues: 1-471 <TAS>
A; Cross-references: GB: 1.05404
A; Cross-references: GB: 1.05404
A; Note: it is uncertain whether Met-1 or Met-51 is the initiator
A; Note: intron positions were determined from partial DNA sequence
R; Luee, JJ; von Kessler, D.P.; Parks, S; Beachy, P.A.
Cell 71, 33-50, 1992
A; Title: Secretion and localized transcription suggest a role in positional signaling
A; Reference number; A43480; MUID: 93008241
A; Accession: A43480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S66384; NID:g435848; PID:g435849
A;Experimental source: Oregon-R
A;Experimental source: Oregon-R
A;Note: Sequence extracted from NCBI backbone (NCBIN:138996, NCBIP:138997)
R;Tashiro, S.; Michiue, T.; Higashijima, S.; Zenno, S.; Ishimaru, S.; Takahas
Gene 124, 183-189, 1993
A;Title: Structure and expression of hedgehog, a Drosophila segment-polarity
A;Reference number: JN0501; MUID:93185922
A;Accession: JN0501
                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Superfamily: sonic hedgehog protein
C:Keywords: transmembrane protein
F:62-82/Domain: transmembrane #status predicted <TWM>
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A:Introns: 160/3; 248/1
C:Superfamily: sonic hedgehog protein
C:Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
A; Gene: hh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:L02793; NID:g157609; PID:g157610
A;Note: sequence extracted from NCBI backbone (NCBIP:115418)
C;Comment: This protein is required for cell-cell communicat
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A; Residues: 1-471 <LEE>
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A;Molecule type: mRNA
A;Residues: 1-471 <TAB>
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 189
                                                                                                        130 TEGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWYYYESKAHVHCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 VKSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDR 249
                                                                                                                                                                       125 VIRRDSPKFKDLVPNYNRDILFRDEEGTGADRLMSKRCKEKLNVLAYSVMNEWPGIRLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 APERLIHAL - GALLPGGAVQPTGMHWYSRLLYRLAEELM
                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                   14 LVLLLLLVVP----AAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEG
                                                                                                                                                                                                                                                                                                                                            Local Similarity 45.9 les 189; Conservative
VKSDSSISSHVHGCFTPESTALLESGVRKPLGELSIGDRVLSMTANGQAVYSEVILFMDR 304
                                                                                                                                                                                              KIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRV
                                                                                                                                                                                                                                                           LVALLLIVLPMVFSPAHSCGPGRGLGRHR---ARNLYPLVLKQTIPNLSEYTNSASGPLEG
                                                                                   TESWDEDYHHGQESLHYEGRAVTIATSDRDQSKYGMLARLAVEAGFDWVSYVSRRHIYCS
                                                                                                                                                                                                                                                                                                                                            41.1%; Score 893.5; DB 2;
45.9%; Pred. No. 5.3e-68;
tive 61; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed specifically in posterior compartm
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                                                                                                                                                                                                                                                                                                                                                 31;
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189

184

124 69

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129

Takahashi, F.;

gene

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A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-615 < NHA>
A; Cross-references: EMBL: U88183; PIDN: AAB52656.1; GSPDB: GN00028; CESP: ZK377.1
A; Cross-references: Strain Bristol N2; Clone ZK377
                                                                                                                                                                                                                                                                                                                                         C; Accession: T29550
R; Nhan, M.; Hawkins, J.
submitted to the EMBL Data Library, February 1997
A; Description: The sequence of C. elegans cosmid:
A; Reference number: Z20639
A; Accession: T29550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-94 <DRU>
A;Cross-references: EMBL:U59748; NID:g1401271; PID:g1401272
C;Genetics:
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                                                                                                                                                                  A:Gene: CESP:ZK377.1
A:Map position: 10
A:Introns: 46/1; 70/3; 157/2; 176/1; 245/2; 314/3; 402/3; 499/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: G02735 R; Drummond, I.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        desert hedgehog - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein ZK377.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Species: Caenorhabditis elegans;Date: 15-Oct-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
342 QSGSYSGSYSGYPTADASQYNAYPAMQQPAYQPAYQPAYQPAYQPAYQPAYQPAYQPAYSARGY 401
                                     142 ESLHYEGRAVDITTSDRDR-NKYGLLARLAVEAGFDWVYYES-KAHVHCSVKSEHSAAAK 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 RAVDITTSDRDRNKYGLLARLAVEAGFDWVYYES 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 HSLAWGSWTPGE-------GVHWYPQLLYRLGRLLLEEGSFH 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 EPHRLRAFQVIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQPGQYVLVAGV
                                                                           Local Similarity 24.7 ses 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETGELRPQRVVKVGSVRSKGVVAPLTREGTIVVNSVAASCYAVINSQSLAHWGLAPMRLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                           8.0%;
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                                                                           52;
                                                                         Score 174.5; DB 2;
Pred. No. 7.6e-07;
2; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 456; DB 2; Pred. No. 7.6e-32;
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                                                                                                                                                                                                                                                                                                                                                                                     ZK377
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                                                                                                             Length
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submitted to the EMBL Data Library
A;Reference number: 219716
A;Accession: T23752
A;Status: preliminary; translated
                                                                                                                                                                                                                             RESULT
T23252
                                                                                                                                         hypothetical protein K02E2.2 - Caenorhabditis elegans c;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T23252
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A; Introns: 45/3; 200/1; 235/3; 436/3; 561/3; 581/3; 696/3; 742/1; 826/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-868 <WIL>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Ainscough, R.
submitted to the EMBL Data
A;Reference number: Z19541
A;Accession: T22281
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Molecule type: DNA
A; Residues: 1-1021 <WIL>
                                                                                                                          R;Lloyd,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          571 SLYKRTSSVFHNLMFFKSSTEEG
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                                                                                                                                                                                                                                                                                                             ROKVLNLFGILHMNEIELPTGTAVYKELL 860
                                                                                                                                                                                                                                                                                                                                                 ---PLRLFHSLAWGSWTPGEGVHWYPQLL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETQDPPRRLALTPAHLLFTA-------DNHTEPAARFRATFASHVQPGQYVLVA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCFSSDTLVTTPSGKK-RMDEIDVGDYVLTANR-VKTHFTPVTLWIHRESEKLEEFLTI 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PL-----RLFHSLAWGSWTPGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVVI------KKKVSKISKVIETGIYSPLTSTGDIIVNRVLASCHSNLALKSLQQ-TFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVLVAGVPGLQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFW 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRDEEIAEFNLIETAN-GHSIKLTDNHLIYVSDCRTRSDLKLVAAKEVKMDDCIHVTTDS 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPHRLRAFQVIETQDPPRRLALTPAHLLFTADNHTE-----PAARFRATFASHVQPGQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPNLNGLFGGTGMQCFSGDMEVETEDGIKM-IKDLKIGDKVLSM-DEAFVTYSPVIMFLH
                                                                                                                                                                                                                                                                                                                                                                                            ENTKFRQEKINQTTRGLKTGIYSPLTKNGRIIVNDMLASCYSEVQANVLQTTYFWVFNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                     GVPGLQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TTERGSTLQLTPLHFMYRTKCNESSEFLKILPENH-----EAILASYLEIGDCVILT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 26.3
55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: Z81540; PIDN: CAB04405.1; GSPDB: GN00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone F46B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.0%; Score 173.5; DB 2;
26.3%; Pred. No. 1.5e-06;
tive 33; Mismatches 90;
                                                                                                  Library,
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                                                                                                     November
                                        GB/EMBL/DDBJ
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A;Cross-references: EMBL:Z81560; PIDN:CAB04547.1; GSPDB:GN00023; CESP:K02E2.2 A;Experimental source: clone K02E2 C;Genetics:
hypothetical protein T05C12.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C;Accession: T23754; T24513
                                                                                                RESULT
T23754
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A;Map position: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1226 <WIL>
A; Cross-references: EMBL: 268008; PIDN: CAA92000.1; GSPDB: GN00028; CESP: R08B4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, November 1995 A; Reference number: Z19834 A; Accession: T24045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein R08B4.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T24045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 53/2; 113/1; 152/3; 204/3; 272/1; 354/1; 389/3; 714/3; 839/3; 877/1; 960/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 7.4%; Score 161; DB 2; Best Local Similarity 25.0%; Pred. No. 2.7e-05; Matches 43; Conservative 39; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.8%; Score 170.5; DB 2
Best Local Similarity 24.3%; Pred. No. 3.3e-06;
Matches 55; Conservative 42; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                1133 KYRQQKIETITRSVRTGIYSPLTNNGRIIVNDMLASCYSEIQQNTLQTTFFW 1184
                                                                                                                                                                                                                                                                                                  1074
                                                                                                                                                                                                                                                                                                                                                                                           1016 AATGACFSLDTWVTTPTGKK-RMDQIDIGDYVLTADLE-KTYFTPITLWIHREPEKVQEF 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              860
                                                                                                                                                                                                                                                                                                                                                258
                                                                                                                                                                                                                                                                                                                                                                                                                                        198 AKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREPHRLRAF 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 CFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREPHRLRAFQVIET 262
                                                                                                                         15
                                                                                                                                                                                                                                             GLQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFW 362
                                                                                                                                                                                                                                                                                                LTIMT-EYGKTLRITSRHFMYRNKCGKSYPQYIKMLPHDGEAIFASDLEVGDCVVVLYKG 1132
                                                                                                                                                                                                                                                                                                                                           QVIETQDPPRRLALTPAHLLF---TADNHTEPAARF----RATFASHVQPGQYVLVAGVP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDPPRRLALTPAHLLFTADNHTEPA------ARFR------ATFASHVQPG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WAFDRLRNL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -DNGKTLQLTAGHFIYATECRYLPSKNSSLLNSTPERYRHLIDTLPDDSETKLASQLKIG 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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R;Thomas, K.
submitted to the EMBL Data Library,
A;Reference number: Z19793
A;Accession: T23754
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A; Introns: 31/3; 87/2; 141/3; 180/2; 203/3; 267/1; 776/2; 794/2; 834/2; 1086/3; 1143/
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP:T05C12.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:Z66500; PIDN:CAA91313.1; GSPDB:GN00020; CESP:T05C12
A;Experimental source: clone T05C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1207 <WI2>
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A;Residues: 1-1207 <WIL>
A;Cross-references: EMBL:Z49968; PIDN:CAA90265.1; GSPDB:GN00020; CESP:T05C12.10
A;Experimental source: clone M110
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A; Residues: 1-1207 <
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Best Local Similarity 28.29
                                                                         1068
                                                                                                                                                     1009
1128 F 1128
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                                   361
                                                                                         196 AAAKTGG----CFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREP 251
                                                                       ECVLSIDESGEVIADEIVRVGRMTNVGIYSPMTVEGSLIVDGVLSSCFSHLESHSAHKLI 1127
                                                                                                                                                 KTRTNFVVLYTKS-GRKLSLTGRHLLPVAECSQVEQYTMNPDGIDVAMRESKYAEKARKG
                                                                                                                                                                                     HRLRAFQVIETQDPPRRLALTPAHLL-----FTADNHTEPAARFRATFASHVQPG 301
                                                                                                                                                                                                                           AAGAAGGGRSNCFSADSLVTTVTGQK-RMDELQIGDYVLVPSSGNVLKYEKVEMFYHREP
                                                                                                                                                                                                                                                                                                                         7.18;
28.28;
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                                                                                                                                                                                                                                                                                                     ; Score 154.5; DB 2;
; Pred. No. 9.5e-05;
30; Mismatches 83;
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Match
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    83857 seqs, 30454973 residues
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Gapop 10.0 , Gapext 0.5
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THL_BRARE
DHL_MOUSE
DHL_HUMAN
DH12_XENLA
DH11_XENLA
HH_DROMY
SHH_CARAU
SHL_PUNTE
SHL_TANAL
SHL_RASEL
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SHH_CHICK
                     SHH_DEVDE
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P97812 mus musculu
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5 cynops pyrr
xenopus lae
3 rattus nory
brachydanio
brachydanio
8 mus musculu
homo sapien
1 xenopus lae
6 drosophila
4 drosophila
1 carassius a
puntius tet
tanichthys
2 amblypharyn
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Result No.

45	44	43	42	41	40	39	38	37	36	35
290	290	295	295	295	295	295	295	295	546	548
13.3	13.3	13.6	13.6	13.6	13.6	13.6	13.6	13.6	25.1	25.2
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79712	79729	79860	79852	13243	79719	P79711	13240	79693	79838	79864
danio kerri	brachydanio	rasbora ele	puntius tet	devario dev	danio pulch	danio kerri	danio aff.	carassius a	puntius con	rasbora het

## ALIGNMENTS

888888888	4888888888888888	7	SOO S R R R R R R R R R R R R R R R R R	RES IHH AC DT DT DT DT DE GN
-!- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).	Development 120:3339-3353(1994).  -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENT'S DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. INDUCES THE EXPRESSION ENDOCHONDRAL OSSIFICATION. MAY REQULATE THE BALANCE BETWEEN GROWTH AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION OF PARATHYROID HORMONE-RELATED PROTEIN (PTHRP) (BY SIMILARITY).  -!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).  -!- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC LUNG, AND IN ADULT KIDNEY AND LIVER.	Marigo V., Roberts D.J., Lee S.M.K., Tsukurov O., Levi T., Marigo V., Roberts D.J., Gilbert D.J., Copeland N.G., Seidman C.E., Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C.; "Cloning, expression, and chromosomal location of SHH and IHH: two human homologues of the Drosophila segment polarity gene hedgehog."; Genomics 28:44-51(1995). [3] SEQUENCE OF 124-172 FROM N.A. MEDLINE; 95236997. Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.; "Products, genetic linkage and limb patterning activity of a murine hedgehog gene.";	Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  [1]  SEQUENCE FROM N.A.  Tate G., Endo Y., Mitsuya T.;  "Human Indian Hedgehog.";  Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.  [2]  SEQUENCE OF 100-411 FROM N.A.  TISSUB-FETAL LUNG;  MENTINE, ACCORDAN	RESULT 1  IHH_HUMAN STANDARD; PRT; 411 AA.  ID IHH_HUMAN STANDARD; PRT; 411 AA.  AC Q14673; 043322;  DT 15-JUL-1999 (Rel. 38, Created)  DT 15-JUL-1999 (Rel. 38, Last sequence update)  DT 15-JUL-1999 (Rel. 38, Last sequence update)  DT 15-JUL-1999 (Rel. 38, Last annotation update)  DE INDIAN HEDGEHOG PROTEIN PRECURSOR (IHH) (HHG-2).  GN IHH.

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RESULT 2
IHH_MOUSE
ID IHH_MOUSE
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EMBL; AB018075; BAA33523.1; JOINED.
EMBL; AB010092; BAA33523.1; JOINED.
EMBL; L38517; AAA62178.1; -.
MIM; 600726; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatis the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
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                                                                                  FWPLRLFHSLAWGSWTPGEGVHWYPQLLYRLGRLLLEEGSFHPLGMSGAGS
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                                                                    FWPLRLFHSLAWGSWTPGEGVHWYPQLLYRLGRLLLEEGSFHPLGMSGAGS
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IIL -> LIF (IN REF. 2).
F -> V (IN REF. 2).
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INDIAN HED
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INDIAN HEDGEHOG PROTEIN N-PRODUCT.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER (
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SWISS-PROT entry is copyright. It is produced through a collaboration -

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RL Development 120:3339-3353(1994).

RE Development 120:3339-3353(1994).

C -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: BINDS TO THE PATCHED (PTC)

C RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN ENDOCHONDRAL OSSIFICATION: MAY REGULARE THE BALANCE BETWEEN GROWTH OF THE DEVELOPING BONES: INDUCES THE EXPRESSION OF PARACHYROID HORMONE-RELATED PROTEIN (PTHRP).

C -!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL SUBCELLULAR IN "TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SUBCACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

C -!- TISSUE SPECIFICITY: IN THE EMBRYO, DETECTED IN THE DEVELOPING GUT, THE GROWTH ZONE OF CARTILAGE OF DEVELOPING LONG BONES, EPITHELIUM CAND URGGENITAL SINUS. IN THE ADULT KIDNEY, FOUND IN PROXIMAL CONVOLUTED AND PROXIMAL STRAIGHT TUBULE.

C -!- DEVELOPMENTAL STAGE: DETECTED AT 10 DAYS POST COITUM (DPC) IN DEVELOPING GUT, AT 14.5 DAYS DPC IN THE CARTILAGE PRIMORDIUM AND IN THE DEVELOPING URGGENITAL SINUS. EXPRESSION INCREASES WITH GESTIONAL AGE IN KIDNEY AND DUODENUM, BECOMING MAXIMAL IN ADULT HOUSE.
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15-JUL-1999 (Rel. :
15-JUL-1999 (Rel. :
15-JUL-1999 (Rel. :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang D.T., Lopez A., von Kessler D.P., Cl
Zhao R., Seldin M.F., Fallon J.F., Beachy
"Products, genetic linkage and limb patter
hedgehog gene.";
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MEDLINE; 97236802.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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ADULTHOOD.

PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOLETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY), SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
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PROTEIN PRECURSOR (IHH) (HHG-2).
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Q98938;
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CONFLICT
SEQUENCE
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SITE
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PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
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EMBL; X76291; CAA53923.1; -.
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Gallus gallus
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HEDGEHOG PR
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 (Chicken)
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                     1. 38, Created)
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PROTEIN PRECURSOR (IHH).
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Pred. No. 2.1e-1
0; Mismatches
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W -> S (IN REF. 2).
; 08BE7AD8507C0D9B CRC64;
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INVOLVED IN CHOLESTEROL TRANSFER (BY
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INDIAN HEDGEHOG PROTEIN
INDIAN HEDGEHOG PROTEIN
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OF PARATHYROID HORMOR-RELATED PROTEIN (PTHEP).

-!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL, UNFROME IS ALSO SECRETED IN ETHHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING MIDGUT, LUNG AND CARTILAGE OF DEVELOPING LONG BONES IN THE LIMB.

-!- PTM. THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTECLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT AUTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEMLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
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Tabin C.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and PTH-related protein.";
Science 273:613-622(1996).
-i- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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EMBL; U58511; AAC60010.1; -. PFAM; PF01079; Hint; 1. PFAM; PF01085; HH\_signal; 1. PRINTS; PR00632; SONICHHOG

Developmental protein; Autocatalytic cleavage; Hydrolase;

BINDING CHAIN CHAIN CHAIN SITE SITE Signal SIGNAL SITE ACT\_SITE 198 408 1 24 24 199 198 244 271 ΑĄ; 23 408 198 408 199 244 198 271 268 44829 M. INDIAN HEDGEHOG PROTEIN.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER () CHOLESTEROL (BY SIMILARITY).
BA397AE2A9357A24 CRC64; ESSENTIAL FOR SIMILARITY). SIMILARITY) INVOLVED IN AUTO-CLEAVAGE FOR AUTO-CLEAVAGE (BY

Query Match Best Local S Matches 320 Similarity 75.7%;
nilarity 77.7%;
Conservative 2: Score 1645.5; Pred. No. 7.8e Pred. Mismatches 5; DB 1; .8e-131; Indels Length 408; ហ Gaps

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δÃ 밁 Š 61 - $\vdash$ MSPARLRPRLHFCLVLLLLLVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKT 60 LGASGRYEGKIARSSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMN MKPARLLLLLSGC----ALLLAPAVRCCGPGRVVGSRRRPPRKLIPLAYKQFSPNVPEKT 56

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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INDIAN HEDGEHOG PROTEIN PRECURSOR (IHH) (BANDED
   This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                       PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NOTERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES INMBOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY). SHALLARITY: BELONGS TO THE HEDGEIOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE: DETECTABLE WITHIN THE EARLY GASTRULA, AT STAGE 14 NEURULA, HIGH EXPRESSION IN NEUROECTODERM. EXPRESSED THROUGHOUT THE NEURAL PLATE AND SUBSEQUENTLY IN BOTH THE NERVOUS SYSTEM AND IN THE DERWATOME OF SOMITES.
INDUCTION: BY ACTIVIN.
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                                                                                                                                SHH_MOUSE STANDARD;
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15-JUL-1999 (Rel. 38, La
15-JUL-1999 (Rel. 38, La
SONIC HEDGEHOG PROTEIN P
SHH OR HHG1.
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO
                                                                                      Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                     Eutheria;
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99; Mismatches
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INDIAN HEDGEHOG PROTEIN C-PRODUCT
INDIAN HEDGEHOG PROTEIN C-PRODUCT
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE (BY
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ESSENTIAL FOR AUTO-CLEAVAGE
                                                                                      Craniata;
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                                                                     Muridae;
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ches 74;
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ae; Murinae;
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-!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-!- TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF EMBRYONIC TISSUES INCLUDING THE NOTOCHORD, VENTRAL MEURAL TUBE, FLOOR PLATE, LUNG BUD, ZONE OF POLARIZING ACTIVITY AND POSTERIOR DISTAL MESENCHYME OF LIMBS. IN THE ADULT, EXPRESSED IN LUNG AND NEURAL RETINA.

-!- DEVELOPMENTAL STAGE: FIRST DETECTABLE DURING GASTRULATION.

-!- INDUCTION: BY RETINOLD ACTIVITY. BOTH ACTIVITIES RESULT IN ADD A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CHAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE CALBURANT OF THE CONTROL OF THE CON
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"A potential catalytic site revealed by the 1.7-A crystal structure
the amino-terminal signalling domain of Sonic hedgehog.";
Nature 378:212-216(1995)
-i- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS 1
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Beachy P.A., Jessell T.M.;

"Floor plate and motor neuron induction by different concentrations

"Floor plate and motor neuron foundation by different concentrations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sonic hedgehog, a member of a family of putative molecules, is implicated in the regulation of CNS cell 75:1417-1430(1993).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Submitted (NOV-1997)
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Echelard Y., Epstein D.J., St Jacques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCCENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL FOR A UNITED THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR ANIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE-AND MOTOR NEURON-INDUCTING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
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                                                                                                                                                                                                                                                       C-PRODUCT HAS NO SIGNALING ACTIVITY. SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
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R., Seldin M.F., Fallon J.F., Beac
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SHH_BRARE STANDARD; PRT; 418 AA. 092008; 013170; 013171; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) SONIC HEDGEHOG PROTEIN PRECURSOR (SHH) (VHH-1).
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SONIC HEDGEHOG PROTEIN N-PRODUCT SONIC HEDGEHOG PROTEIN C-PRODUCT CLEAVAGE (AUTO-) (BY SIMILARITY)
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Closely related to the zebrafish.;

Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).

-I. FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHENED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (DORSO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
                                                                                                                                                                                                                                                                                                        -I- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL SURFACE: A "TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE: IS ALSO SECRETED IN EITHER CLEAVED ON UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-I- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL TUBE AND BRAIN. ALSO FOUND IN THE VOTOCHORD AND IN DEVELOPING FIN BUD. IN THE DEVELOPING BRAIN. EXPRESSION OCCURS IN DOMAINS THAT INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DIENCEPHALON.

-I- DEVELOPMENTAL STAGE: FIRST DETECTABLE IN THE INER CELL LAYER OF THE EMBRYONIC SHIELD DURING GASTRULATION. BY 9.5 HRS OF DEVELOPMENT, EXPRESSED IN A CONTINUOUS BAND THAT EXTENDS FROM THE PRESUMPTIVE MIDBAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 96083328.
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Moon R.T., Beachy P.A.;
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Ruiz I Altaba A., Tanabe Y.,
Dodd J.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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PIM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NOTERMINAL FRAGMENT (N-PRODUCT). THIS COVALENY MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
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, Jessell T.M.,
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U30711; AACS9742.1;

U355669; CAAA4738.1;

U51351; AAB38575.1;

U51370; AAB38593.1;
                                                       LVAGVPG-LQPARVAAVSTHVALGAYAPLTKHGTLVVEDVVASCFAAVADHHLAQLAFWP
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                                                                                                         IFLDREPHRLRAFQVIETQDPPRRLALTPAHLLFTADNHTEPAARFRATFASHVQPGQYV
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                                            GRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMNHWPG
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                                                                                                                                        HIHCSVKAENSVAAKSGGCFPGSALVSLQDGGQKAVKDLNPGDKVLAADSAGNLVFSDFI
                                                                                                                                                                                      VKLRVTEGWDEDGHHFEESLHYEGRAVDITTSDRDKSKYGTLSRLAVEAGFDWVYYESKA
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s; PR00632; SONICHHOG.
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61.2%;
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SONIC HEDGEHOG PROTEIN C-PRODUCT.
SONIC HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-).
INVOLVED IN CHOLESTEROL TRANSFER
                                                                                                                                                                                                                                                                                                                                         Score 1274; DB 1;
Pred. No. 1.3e-99;
                                                                                                                                                                                                                                                                                                                                                                                                           ESSENTIAL FOR AUTO-CLEAVAGE SIMILARITY).
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CF000AFFFD2F5795 CRC64;
                                                                                                                                                                                                                                                                                                                              Mismatches
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OF THE NEURAL TUBE.

-!- DEVELOPMENTAL STAGE: FIRST DETECTABLE AT STAGE 17 DURING THE INITIATION OF LIMB BUD FORMATION. FROM THAT POINT ONWARDS, THE EXPRESSION PATTERN EXACTLY MATCHES THE LOCATION OF THE ZONE OF POLARIZING ACTIVITY (ZPA).

-!- INDUCTION: BY RETINOID ACID.
-!- PIM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURRACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AULOPIOLEO19515.";

Cell 81:445-455(1995).

-I - FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARLETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITSS, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE: 95254654.

Roelink H., Porter J.A., Chiang C., Tanabe Y., Chang D.T.,
Beachy P.A., Jessell T.M.;

"Floor plate and motor neuron induction by different concentrations
the amino-terminal cleavage product of sonic hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 94094333.

**Riddle R.D., Johnson .L., Laufer E., T
"Sonic hedgehog mediates the polarizing cell 75:1401-1416(1993).

[2]

FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE.
                                     Signal.
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SONIC HEDGEHOG PROTEIN PRECURSOR (SHH).
                                                                      Developmental
                                                                                                      PFAM;
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TISSUE SPECIFICITY: EXPRESSED IN THE NOTOCHORD, AND THE FLOOR PLATE MESSENCHYME, THE HENSEN'S NODE, THE NOTOCHORD, AND THE FLOOR PLATE
                                                                                                                                                                                                                                                                                                   C-PRODUCT HAS NO SIGNALING ACTIVITY.
SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                    L28099; AAA72428.1; -. PF01079; Hint; 1. PF01085; HH_signal; 1. S; PR00632; SONICHHOG.
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27
27
                                                                                                                                                                                                                                                                                                                    HAS NO SIGNALING
                                                                    protein; Autocatalytic cleavage;
     26
425
200
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ne polarizing activity
POTENTIAL.
SONIC HEDGEHOG PROTEIN.
SONIC HEDGEHOG PROTEIN N-PRODUCT.
                                                                    Hydrolase; Protease;
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EQUENCE	EQUENCE EQUENCE ISSUE-FEEDLINE; arigo V. astier Jenkins N Cloning, man homemores	HH. omo sapi okaryota otheria;	5-JUI 5-JUI 5-JUI	T 8	373 G 378 ALCP	314 PARVA      318 PASVH	260 IETQ    : 258 IETR	200 TGGCF :     198 SGGCF	140 SEES      138 SEES	80 ELTPNYNPI         78 ELTPNYNPI	20 LVVP.  :  19 LLVS	ery Match st Local S ches 257	BINDING DOMAIN SEQUENCE	ACT_SITE	ITE	SITE SITE
1 107	WCE FROM N.A. 2-FETAL LUNG; RS; 96070431. D V., Roberts D.J. ST J.M., Epstein I S N.A., Seidman G. Ing, expression, a homologues of the homologues of the	EHOG PRO  ns (Huma  Metazoa  Primates	99 (Rel 99 (Rel 99 (Rel	S	DGAIPTAAT	AVS-	DPPRRLALT           QPRARLLLT	GCFPAGAQVRI	LHYEGRAVI          LHYEGRAVI	NYNPDIIFK          NYNPDIIFK	PAAWGCGPGRVVGS :       :  SSGLTCGPGRGIG-	imilarity ; Conser	200 390 425 AA;	273	270	201 200 246
1	J.G., Le	രറ് ∺	8, Creat 8, Last 8, Last	TANDARD;	-SWIPGEGVHWYP :    :   TAATTTTGIHWYS	GAYAPLI          GAYAPLI	IETQDPPRRLALTPAHLLETADNHTEPAA    :                    ETRQPRARLLLTAAHLLEVAPQHNQSEATGST	PAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREPHRLRAFQV 	EESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHSAAAK 	DIIFKDEENTGADRLMTQRCKDRLNSLAISVANQWPGVKLRVTEGWDEDGHH 	VVGSRRRPF :  :     GIG-KRRHF	58.4%; 63.0%; vative	200 393 46474 M	273	270	425 201 246
	e S.M.K., Gilbert McMahon hromosoma sophila s	URSOR (SHH) la; Craniata lini; Homini	Created) Last sequence Last annotatio	PRT;	PQLLYRLGRLLLEEGSFHPLGMSGA            :  :         SRLLYRIGSWVLDGDALHPLGMVAP	CKHGTLVVEDVVA     :::  :    AQGTILINRVLA	)NHTEPAA   ;   OHNQSEATG	SAVRPGDRVI :        (DLSPGDRVI	KYGLLARL <i>I</i>    :      KYGMLARL <i>I</i>	LMTQRCKDE	GSRRRPPRKLVPLAYF   :    :        G-KRRHPKKLTPLAYF	Score 12 Pred. No 38; Misma	CHOLESTEROL POLY-THR. MW; DA9627443	SIMILAR ESSENTI	INVOLVE	SONIC F
	Tsul D.J. A.P. 11 loosegmen	) (HHG a; Ver idae;	date) updat	462 AA.	VVLDGDALH	/VASCEAAV  :  : : : /LASCYAVI	RFRATFA:           STSGQALFA:	PGDRVLAMGEDGSPTFSDVLIFLDREPHRLRAFQV          GDRVLAADADGRLLYSDFLTFLDRMDSSRKLFYV	AVEAGFDWV           AVEAGFDWV	RLNSLAISV :  :      KLNALAISV	KQFSPNVPEKTI	1270.5; Vo. 2.6e-	ESTEROL (BY STITHR.)627443D4A017	RITY). [AL FOR A	ED IN AUTO-	SONIC HEDGEHOG P CLEAVAGE (AUTO-) INVOLVED IN CHOL
	<pre>curov O., Lev Copeland N. Tabin C.; Tabin of SH nt polarity g</pre>	1). ebrata;	تد		IPLGMSGAG      IPLGMVAPA	AAVADHHLAQLAF   : :       AVIEEHSWAHWAF	SHVQPG  : :	TESDVLIF           LYSDFLTF	YYESKAHV      :  YYESKAHI	MNQWPGVK	KTLGASGRY           KTLGASGRY	DB 1; 99; 96; I	SIMILARITY	TO-	O-CLEAVAGE	OG PROTEIN C-PROTO-) (PROBABLE). CHOLESTEROL TRAN
	i T G., and	Mammalia			AS 425	AFWPLRLF          AFAPFRLA	QYVLVAGVF 	LDREPHRI	HCSVKSEH	LRVTEGWE	(YEGKIARSSERFF        :       YEGKITRNSERFF	ngth 4 els	(ITY).	CLEAVAGE (BY	GE (BY	isi du
	Seidman C.I IHH: two hedgehog."	<del></del>				HSLAW      QGLLA	£ :	N N			SERFK 79	25; 17; Gaps		•		ER (BY
	·					372 377	314 317	59 57	199 197	139 137	7 9	w				

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TSUÍ L.-C., Muenke M.;

"Mutations in the human Sonic Hedgehog gene cause holoprosencephaly.";

RL Nat. Genet. 14:357-350(1996).

10. -1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO). TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER ACTIVITY OF SMO. ALSO REGULATES ANOTHER TOR A CONSTITUTIVE SIGNALING EVENTS DURING DEVELOPMENT: SIGNAL FOR A CONSTITUTIVE SIGNAL INDUCES DURING DEVELOPMENT: SIGNAL FOR A CONSTITUTION OF THAT INDUCES VENTRAL CELL FATE IN THE MEURAL TUBE OF THE MOTOCHORD THAT INDUCES VENTRAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE-AND MOTOR NEUBRON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEUBRON INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEUBRON INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE INDUCTION (BY STATE DEVELOPING LIMB BUD. DISPLAYS BOTH CLOOR PLATE STATE DEVELOPING 
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1- DISEASE: DEFECTS IN SHH ARE THE CAUSE OF THE AUTOSOMAL DOMINANT DISCRADER HOLOPROSENCEPHALY TYPE 3 (HPE3). HPE3 IS A GENETICALLY HETEROGENEOUS DISEASE THAT AFFECTS THE MIDLINE DEVELOPMENT OF THE FOREBRAIN AND MIDFACE. HPE IS ASSOCIATED WITH SEVERAL DISTINCT FACIES AND PHENOTYPIC VARIABILITY. IN THE MOST EXTREME CASES, ANOPHTHALMIA OR CYCLOPIA IS EVIDENT ALONG WITH A CONGENITAL ABSENCE OF THE MATURE NOSE. THE LESS SEVERE FORM FEDTURES FACIAL DISCRETARING OF THE MATURE NOSE. THE LESS SEVERE FORM FEDTURES FACIAL DISCRETARING OF THE MATURE NOSE. THE LESS SEVERE FORM FEDTURES FACIAL DISCRETARING OF THE MATURE NOSE. THE LESS SEVERE FORM FEDTURES FACIAL DISCRETARING OF THE MATURE NOSE. THE LESS SEVERE FORM FEDTURES FACIAL DISCRETARING OF THE MATURE OF T
                                                                                                        EMBL; L38518; AAA62179.1; -.
EMBL; AC002404; AAB67604.1; -.
EMBL; AC002404; AAB67604.1; -.
MIM; 600725; -.
MIM; 142945; -.
MIM; 142945; -.
MIM; PF01079; Hint; 1.
PFAM; PF01079; Hint; 1.
PFAM; PF01085; HL_Signal; 1.
PRINTS; PR0032; SONICHHOG.
Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bidinformatics and the EMBL outstation the European Bidinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORPUS CALLOSUM.
-!- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
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Roessler E., Belloni E., Gaudenz K., Jay P., Berta P., Scherer S.W.,
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SUBCELULIAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN FETAL INTESTINE, LIVER, LUNG, AND KIDNEY. NOT EXPRESSED IN ADULT TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UPPER LIP AND/OR NOSE, AND ABSENCE OF THE OLFACTORY NERVES OR
Disease mutation.
1 23
24 462
    POTENTIAL.
SONIC HEDGEHOG PROTEIN.
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RESU SHH_ ID AC DT DT DT DT DT DT DT DT DT DT DT DT DT	Qy Q	O 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
ULT 9 SHLCYNPY Q90385; 15-JUL-199 15-JUL-199 SONIC HEDG SHH, Cynops pyr Eukaryota; Batrachia; [1] SEQUENCE F TISSUE-EMB MEDLINE; 9	ery Matc st Local tches 2 13 Cl 7 Cl 7 Cl 131 EG 131 EG 191 KS 191 KS 196 KA 255 AS 295 AS 295 AS 295 AS 295 AS 295 AS	CHAIN CHAIN SITE SITE SITE ACT_SITE BINDING DOMAIN VARIANT VARIANT VARIANT VARIANT
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) ebrata; Amphibia; ridae; Cynops.	Length 462; Indels 59; G TOPEKTLGASGRYEGK	PROTEIN N-PRODUCT. PROTEIN C-PRODUCT. ) (BY SIMILARITY). )LESTEROL TRANSFER (BY CO-CLEAVAGE (BY AUTO-CLEAVAGE (BY  C SIMILARITY).  2 SIMILARITY).  3). 10. 11. 11. 12. 13. 14. 15. 16. 17. 18. 18. 18. 18. 18. 18. 18. 18. 18. 18
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SEQUENCE
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CHAIN
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SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURPACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

INDUCTION: ACTIVATED BY ACTIVIN, BASIC FIBROBLAST GROWTH FACTOR (BFGF) AND FORK HEAD.

PIM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LEMGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NOT A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NOT A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NOT A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NOT A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE MODIFICATION APPEARS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: ÎNTERCELLULAR SIGNAL ESSENTIĂL FOR A VARIETY OF PAȚTERNING EVENTS DURING DEVLOPMENT AND METAMORPHOSIS. INVOLVED IN LIMB FORMAȚION, PAȚTERNING OF THE CENTRAL NERVOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS. BINDS TO THE PAȚCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
                                                                                                                                                LVPSGLSCGPGRGIGTRKR-FKKLTPLAYKQFTPNVPEKTLGASGRYEGKITRNSERFK 77
                                                                                                                                                                        LVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGKIARSSERFK 79
                   SEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWVYYESKAHVHCSVKSEHSAAAK 199
FEESLHYEGRAVDITTSDRDRSKYGMLARLAAEAGFDWVYFESKAHIHCSVKAENSVAAK 197
                                                                                                ELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGWDEDGHH 139
                                                                         ELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEDGHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D63339; BAA09657.1; -. PF01079; Hint; 1. PF01085; HH_signal; 1. S; PR00632; SONICHHOG.
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ap explants.";
Biophys. Res. Commun. 218:395-401(1996).
                                                                                                                                                                                                                                                                                                                        200
432 /
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27
201
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268
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                                                                                                                                                                                                                                                                                                                          47847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Autocatalytic cleavage;
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                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
SONIC HEDG
SONIC HEDG
SONIC HEDG
CLEAVAGE (
INVOLVED I
                                                                                                                                                                                                                         Score 1263; DB 1;
Pred. No. 1.1e-98;
B; Mismatches 89
                                                                                                                                                                                                                                                                                                                                          CHOLESTEROL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                              ESSENTIAL FOR AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                                        B455C7E746C8E5A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 HEDGEHOG PROTEIN.
HEDGEHOG PROTEIN N-PRODUCT.
HEDGEHOG PROTEIN C-PRODUCT.
HEDGEHOG PROTEIN C-PRODUCT.
AGE (AUTO-) (BY SIMILARITY).
VED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogawa
ead and
                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Protease;
                                                                                                                                                                                                                                                               Length 432;
                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                         Gaps
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         RESULT 10
SHH_XEM
ID SHH_XEM
AC Q9200
DT 15-UD
DT 15-UE
DE SON.
GN SHH.
OS Xenop
OC Batra
RC TISSU
RX MEDLI
RA MOON
RT "Venc
RT "Venc
RT "LSU
RX MEDLI
RX ME
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92000; 091894;
15-7UL-1999 (Rel. 38, Created)
15-7UL-1999 (Rel. 38, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation updat
15-FEB-2000 (Rel. 39, Last annotation updat
15-FEB-2000 (Rel. 39, Last annotation updat
                                                                                                                                                                                                                                                                                              RRUIZ I Altaba A., Jessell T.M., Roelink H.;

"Restrictions to floor plate induction by hedgehog and winged-hel
genes in the neural tube of frog embryos.";

Mol. Cell. Neurosci. 6:106-121(1995).

-i- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOL
IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM A
VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND
FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WH
FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE T
TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC
REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKKET S.C., McGrew L.L.,
Moon R.T., Beachy P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stolow M.A., Shi Y.-B.; "Xenopus sonic hedgehog as a potential morphogen during embryogenesis and thyroid hormone-dependent metamorphosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Distinct expression and shared gene family of Xenopus laevis."; Development 121:2337-2347(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-EMBRYO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDLINE; 95357169
CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN ETTHER CLEAVED OR UNCLEAVED TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: STONGLY EXPRESSED IN NOTOCHORD AND NEURAL FLOOR PLATE DURING EMBRYOGENESIS. IN TAPPOLE, HIGH EXPRESSION OBSERVED IN PANCREAS/STOMACH, MODERATE EXPRESSION IN TAIL, AND EXPRESSION IN INTESTINE, BRAIN, AND HIND LIMB.

DEVELOPMENTAL STAGE: FIRST DETECTED AT THE NEURULA (STAGES 16-
                                                                                                                                                                                                                 SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLGILSFFSPQDYSSHSPPAPSQSEGVHWYSEILYRIGTWVLQEDTIHPLGMAAKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IETQDPPRRLALTPAHLLFTADNH-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acids Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FHSLAWGSWTP----GEGVHWYPQLLYRLGRLLLEEGSFHPLGMSGAGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a; Chordata; Craniata; Vertebrata;
Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23:2555-2562(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       С.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activities of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (X-SHH) (VHH-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TEPAARFRATFASHVQPGQYVLVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               members of the hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          von Kessler D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and winged-helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR, WHICH
         (STAGES 16-17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INVOLVED
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L39213; AAC42227.1; -.
EMBL; L39214; AAA85162.1; -.
EMBL; L35248; AAA49981.1; -.
PFAM; PF01079; H1nt; 1.
PFAM; PF01085; HH_signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                      127
        187
                                              191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NOTERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDUCTION: BY THYROID HORMONE. PTM: THE C-TERMINAL DOMAIN DIS
                                                                                                                                                                                                                                                               LLLL-----LVVPAAWGCGPGRVVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIRST PEAK OF EXPRESSION AROUND TADPOLE HATCHING (STAGES 33-40). HIGH EXPRESSION OBSERVED IN INTESTINE AT THE CLIMAX OF MORPHOGENESIS (STAGES 60-62) WHEN INTESTINE EPITHELIAL UNDERGOES
KAENSVAAKSGGCFPAGARVMVEFGGTKAVKDLRPGDRVLSSDPQGNLLYSDFLMFIDQE
                                   KSEHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDRE
                                                                              EGWDEDGHHLEESLHYEGRAVDITTSDRDRSKYGMLGRLAVEAGFDWVYYESKAHIHCSV
                                                                                                   EGWDEDGHHSEESLHYEGRAVDITTSDRDRNKYGLLARLAVEAGFDWYYYESKAHVHCSV
                                                                                                                                                                                   IARSSERFKELTPNYNPDIIFKDEENTGADRLMTORCKDRLNSLAISVMNQWPGVKLRVT
                                                                                                                                                                                                                                            LLLLSFICTLYTPPGLACGPGRGIG-KRRHPKKLTPLAYKQFIPNVAEKTLGASGRYEGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORPHOGENESIS
                                                                                                                                                                ITRNSDCFKELTPNYNPDIMFKDEESTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVT
                                                                                                                                                                                                                                                                                                                                   250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386
394
403
198
                                                                                                                                                                                                                                                                                                                                Conservative
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266
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401
409
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444
198
199
266
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                                                                                                                                                                                                                                                                                                                                             56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Autocatalytic cleavage; Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                               Score 1251.5; DB 1; Pred. No. 1.1e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                         CHOLESTEROL (BY SIMILARITY).
TOSIL -> NSNLCW (IN REF. 3).
DPKTHMILKAVEKVDLE -> ESQDHDLEGRGKWRRLILR
(IN REF. 3).
N -> S (IN REF. 3).
; 73B4E4932FA2EFF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SONIC HEDGEHOG PROTEIN. SONIC HEDGEHOG PROTEIN N-PRODUCT. SONIC HEDGEHOG PROTEIN C-PRODUCT. CLEAVAGE (AUTO-) (BY SIMILARITY). INVOLVED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESSENTIAL FOR AUTO-CLEAVAGE (BY
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                                                                  SIMILARITY)

-!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-!- TISSUE SPECIFICITY: EXPRESSED IN THE NODE, NOTOCHORD, FLOOR PLATE, AND POSTERIOR LIMB BUD MESENCHYME.

-!- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTECLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE C-TERMINAL OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIET TO THE C-TERMINAL OF THE NEBLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SEATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHH_RAT
Q63673;
15-JUL-1999
15-JUL-1999
15-JUL-1999
This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions
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Roelink H., Augsburger A., Heemskerk J., Korzh V., 1
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Eukaryota; Metazoa; Chor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS
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(Rel. 38, Last sequence update)
(Rel. 38, Last annotation updat
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Sciurognathi; Muridae; Murinae;
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E HEDGEHOG
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59.9%;
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PROTEIN PRECURSOR (TW
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Pred. No. 2.7e
10; Mismatches
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C HEDGEHOG PROTEIN N
C HEDGEHOG PROTEIN C
VAGE (AUTO-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neopterygii;
Cyprinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U30710; AAC59741.1; ZFIN; ZDB-GENE-980526-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ekker S.C., Ungar A.R., Porter J.A., Moon R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
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Eukaryota; Metazoa; Chordata; Craniata; Ver
                                                                                                                          SEQUENCE
                                                                                                                                              BINDING
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                                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                   Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NOTERINIAL FRACMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NUMBER O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUBE AND BRAIN. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAT INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DIENCEPHALON. NOT DETECTED IN THE NOTICHORD OR DEVELOPING FIN BUTTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. INVOLVED IN DORSO-VENTRAL PATTERNING OF THE BRAIN AND IN EARLY PATTERNING OF THE DEVELOPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF01085; HH_signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZDB-GENE-980526-41;
PF01079; Hint; 1.
                           Similarity
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416 AA;
     Conservative
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Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Rasborinae; Danio.
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                                                                                                                             46576
                         56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                   Autocatalytic cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greenstein P., von Kessler Beachy P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWHH.
                                                                                                                          WW;
       53;
  Score 1226.5;
Pred. No. 1.2e
53; Mismatches
                                                                                                                          CHOLESTEROL (BY SIN 61EC2218309CFE59
                                                                                                                                                                                                                                              CLEAVAGE (AUTO-).
INVOLVED IN AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                           TIGGY-WINKLE HEDGEHOG
TIGGY-WINKLE HEDGEHOG
TIGGY-WINKLE HEDGEHOG
                                                                                                                                                                       SIMILARITY).
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                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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                                                                                                                                                                                              FOR AUTO-CLEAVAGE
                         , 2e-95;
                                                                                                                                                 (BY SIMILARITY)
                                                  DB 1;
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       Indels
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                                               Length
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                                                                                                                                                                                                                                                (BY
                                                  416;
                                                                                                                                                                                                                                                                                                                                                                                                                   Protease;
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MBL outstation -
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  21;
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RESULT 13
-I. SUBCLIDUAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL JURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OFFICE CELLS (BY SIMILARITY).

-I. TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE NOTOCHORD.

-I. DEVELOPMENTAL STAGE: FIRST DETECTABLE AT THE MID-GASTRULA STAGE.

DISAPPEARS AT THE END OF THE SOMITOGENESIS.

-I. PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTODROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish.";

Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).

-I- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING AND MUSCLE PIONEER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INDIAN HEDGEHOG PROTEIN PRECURSOR (IHH) (ECHIDNA HEDGEHOG PROTEIN).
IHH OR EHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 382:452-455(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 96310864.
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Eukaryota; Metazoa; Chordata; Canilata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 97075114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 113-170 FROM N.A.
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PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
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                                           HHLAQLAFWPLRLFHSLAWGSWT-PGE---
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INDIAN HEDGEHOG PROTEIN C-PRODUCT.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER ()
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sonic hedgehog, a member of a family of putative molecules, is implicated in the regulation of CNS
                                                                                                                                     SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 120-168 FROM N.A. MEDLINE; 95236997.
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aryota; Metazoa; Chordata; Craniata; Vertebrata;
heria; Rodentia; Sciurognathi; Muridae; Murinae;
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SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FOR MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN ADDLT TESTES. NOT EXPRESSED IN
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PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
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; PF01079; Hint; 1.
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S; PR00632; SONICHHOG.
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                                                  ESSENTIAL FOR AUTO-CLEAVAGE SIMILARITY).
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SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHH_HUMAN STANDARD; PRT; 590 AA Q43323; Q15794; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat DESERT HEDGEHOG PROTEIN PRECURSOR (DHH) (HH
                                                                                                                                                                                                                                                                                           "Human desert hedgehog.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY
PATTERNING EVENTS DURING DEVELOPMENT. MAY FUNCTION AS A
SPERMATOCYTE SURVIVAL FACTOR IN THE TESTES. ESSENTIAL F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHH
                   <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * 4 PASILPIC -- CLALLAL ---- SAQSCGPGRGPVGRRRYVRKQLVPLLYKQFVPSMPERTL
                                                                                                                                                                                                                                                                                                                                                                                              Drummond I.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE-KIDNEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM
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                                              SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO "PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-BANGE SIGNALING, WHEREAS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PARLRPRIHECTVLLLLLVVPAAWGCGPGR-VVGSRRRPPRKLVPLAYKQFSPNVPEKTL
               C-PRODUCT H. SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GASGPAEGRYTRGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNM
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               HAS NO SIGNALING ACTIVITY BELONGS TO THE HEDGEHOG
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0; Mismatches 102;
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                                  (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF01079; Hint; 1.
PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
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367 GALLPGGAVQPTGMHWYSRLLYRLAEELL 395
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                              GSWTPG-----EGVHWYPQLLYRLGRLLL 396
                                                                                  EHSAAAKTGGCFPAGAQVRLESGARVALSAVRPGDRVLAMGEDGSPTFSDVLIFLDREPH 252
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                                                              RPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLLHAL--
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177
396 AA;
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%; Pred. No. 4.8e-91;
47; Mismatches 100; Indels
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E -> G (IN REF. 2).
; FCE4FB21972C3AD5 CRC64;
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DESERT HEDGEHOG PROTEIN N-PRODUCT.
DESERT HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
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7: /cgn2_6/ptodata/
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      June 5, 2000, 07:56:48 ; Search time 52.13 Seconds (without alignments) 2969.733 Million cell updates/sec
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1 ATGGCTCTCCTGACCAATCT......CGGAGGAGCTACTGGGCTGA 1191
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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 US-08-176-427B-3
US-08-176-427B-7
US-08-176-427B-7
US-08-356-060A-4
PCT-US95-02315-1
US-08-356-060A-6
US-08-356-060A-7
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US-08-176-427B-3
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US-08-176-427B-3
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Query Match
Best Local Similarity
Matches 1051; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 60 St
CITY: Boston
STATE: MA
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PCT-US95-14418-3	US-08-474-933-1	US-08-125-468-1	US-07-642-734C-3	US-08-458-568A-11	US-08-459-041A-1	US-08-093-453B-1	US-08-690-473-1	US-08-459-383-30	US-08-384-490-30	PCT-US91-07035-9	US-08-458-819-9	US-07-977-434-9	US-08-682-853A-3	US-08-823-516-3	US-08-756-386-3	US-08-599-491-3	US-08-757-653-3
Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 11, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 30, Appl	Sequence 30, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 3, Appli				

## ALIGNMENTS

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ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 227-7400
TELECAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCLI(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
LENGTH: 1190 base portion of the TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: linear
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US-08-356-060A-2
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                              Matches 1051;
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1141
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121 GTGCCGCTACTCTACAAGCAATTTGTGCCCGGGCTGCCAGAGCGGACCCTGGGCGCCAGT
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STRANDEDNESS: both
TOPOLOGY: linear
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14-DEC-1994
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Pred. No. 5e-194;
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US-08-176-427B-7
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APPLICATION NUMBER: US/08/176,
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, METCHEW P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 46,709
REFERENCE/DOCKET NUMBER: HMI-(
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-740
INFORMATION FOR SEC ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08176427B Patent No. 5789543 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.2%;
Best Local Similarity 64.5%;
Matches 701; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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GAGCCGACCGCTGATGACCGAGCGTTGCAAGGAGAGGGTGAACGCTTTTGGCCATTGCCG
                                                                                                                                                                                                                  CTATGCGCGCAAGCAGCTCGTGCCGCCTACTACAAGCAATTTGTGCCCCGGCGTGCCAG
                                                                                                                                                                                                                                                                                                                               CGCTGCTGGTGTGCCCCGGGCTGGCCTGTGGGCCCGGCAGGGGGTTTGGAAAGAGGCGGC 106
                                                                                                                                TTAAGGAACTCACCCCAATTACAACCCCGACATCATTTAAGGATGAGGAAAACACGG
                                                                                                                                                 TCCGGGACCTCGTGCCCAACTACAACCCCGACATCATCTTCAAGGATGAGGAGAACAGTG
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                                                                GAGCAGACCGGCTGATGACTCAGAGGTGCAAAGACAAGTTAAATGCCTTGGCCATCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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RESULT 4
US-08-356-060A-4
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Patent NO. 5844079
GENERAL INFORMATION:
APPLICANT: Ingoham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
                                                                                                                                      TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                       COUNTRY: US
ZIP: 02109
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                                                                                 STATE:
                                                                                                  STREET: 60 St
CITY: Boston
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Best Local Sim
Matches 701;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 CGCTGCTGGTGTGCCCCGGGCTGGGCCTGTGGGCCCGGCAGGGGGTTTGGAAAGAGGCGGC 106
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STRANDEDNESS: bo
TOPOLOGY: linear
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                                                          TCTACTACGAGTCCCGCAACCACGTCCACGTGTCGGTCAAAGCTGATAACTCACTGGCGG
                                                                                                                                                                  TCCGGGACCTCGTGCCCAACTACAACCCCGACATCATCTTCAAGGATGAGGAGAACAGTG
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                                                                                                                                                                                                                                                                                                                                                          TTAAGGAACTCACCCCCAATTACAACCCCGACATCATATTTAAGGATGAGGAAAACACGG
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                                        TCTACTATGAATCCAAAGCTCACATCCACTGTTCTGTGAAAGCAGAAACTCCGTGGCGG
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Pred. No. 1e-79;
0; Mismatches 362;
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24;

Gaps

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RESULT 5
PCT-US95-02315-1
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                                                                                                                                                                                                                                                                                                      APPLICANT: Edlund, TITILE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                     ATTORNEY/AGENT INFORMATION:
NAME: John, P. White
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45375-A-PCT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1103
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the
                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                  APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                            CITY: New York
STATE: New York
           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCGCT 1127
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Edlund, Thomas
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(212) 338-0400 (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                     Jane
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          TCGTGGCGCCGCACAACGACTCCGGGCCCACTCCGGGACCGAGCCCACTCTTCGCCAGCC 1194
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Pred. No. 4.8e-77;
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                                                ; NAME/KEY:
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US-08-356-060A-6
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US-08-356-060A-6
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                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
REFERENCE/DOCKET NUMBER: HMI-006CP
TELEPHONE: (617) 227-400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
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GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1425 base pair
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MOLECULE TYPE:
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STREET: 60 St
CITY: Boston
STATE: MA
COUNTRY: USA
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                                                                                                                       STRANDEDNESS: single
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                                                                                                                                               1425 base pairs
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Best Local S
Matches 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bonifas, Jeanette TITLE OF INVENTION: Mutant Human NUMBER OF SEQUENCES: 23
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CITY: Menlo Park
STATE: CA
COUNTRY: USA
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                                                                                                                                                                                                                                 172
                                                                                                                                                                                                                                                                                                  Local Similarity 61.8 hes 710; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1576 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                18 TCTACTGCCCTTGTGCTGCCTTGGCACTTCTGGCGCTGCCAGCCCAGAGCTGCGGGCCGGG
                                                                                                                                                                               CCGGGGGCCGGTTGGCCGGCGCCATGCGCGCAAGCAGCTGCCGCTACTCTACAA 137
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                   GATCTCCAGAAACTCCGAGCGATTTAAGGAACTCACCCCCAATTACAACCCCCGACATCAT
                                                      GGTGGCAAGGGGCTCCGAGCGCTTCCGGGACCTCGTGCCCAACTACAACCCCGACATCAT
                                                                                                        GCAATTIGTGCCCGGCGTGCCAGAGCGGACCCTGGGCGCCAGTGGGCCCAGCGGAGGGGAG
                                                                                                                                                       CAGGGGGTTCGGGAAGAGGAGGCAC-----CCCCAAAAAGCTGACCCCTTTAGCCTACAA
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                                                                                      GCAGTTTATCCCCAATGTGGCCGAGAAGACCCCTAGGCGCCAGCGGAAGGTATGAAGGGAA
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Hu, Zhilan
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Pred. No. 2.7e-73;
0; Mismatches 370;
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Sequence 10, Application US/08748591
Patent No. 5759811
GENERAL INFORMATION:
APPLICANT: EStein, Ervin
APPLICANT: Hu, Zhilan
APPLICANT: Bonifas, Jeanette
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                                                                                                                                                                                                                                                                                                                                   CGCGCCGCTCACCGCGCACGGGACGCTGCTGGTGAACGATGTCCTGGCCCTCTTGCTACGC 1034
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US-08-748-591-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 0651
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEPEAX: (415) 824-0875
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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498 AGTGGAAGCCGGCTTCGACTGGGTCTACTACGAGTCCCGCAACCACGTCCACGTGTCGGT
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Local Similarity 61.8%;
les 710; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: CA
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STREET: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                           CGAGGGCTGGGACGAAGATGGCCACCACTCAGAGGAGTCTCTGCACTACGAGGGCCGCGC
                                                                                                                                                                                                GTTGAACGCTTTGGCCATCTCGGTGATAAACCAGTGGCCAGGAGTGAAACTGCGGGTGAC
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                                                                                                                                                TGAGGGCTGGGACGACGGCCACCACGCTCAGGATTCACTCCACTACGAAGGCCGTGC 437
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                                                      AGTGGACATCACCACGTCTGACCGCGACCGCAGCAAGTACGGCATGCTGGCCCGCCTGGC
                                                                                       TTTGGACATCACTACGTCTGACCGCGACCGCCAACAAGTATGGGTTGCTGGCGCGCCTCGC
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2200 Sand Hill Road
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US-08-176-427B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                  APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabln, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
                                                                                                            ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1306 GCTCCTGGC 1314
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CITY: Boston
STATE: MA
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                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTAGGGGC 1103
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                                                                                                                                                         02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application
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Best Local Similarity
Matches 692; Conserv
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE,DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
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TOPOLOGY: linear
MOLECULE TYPE: cDNA
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                                                                                                                                                                649 CGGGAACTGCACCGCGAGACTGGGTTTTGGCGGCCGATGCGTCAGGCCGGGTGGTGCCC
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                                                                                                         ACGCCGGTGCTGCTTCCTTGGACCGGGGACTTGCAGCGCCGGGCCTTCATTTGTGGCTGTG
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US-08-356-060A-1
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REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08356060A
Patent No. 5844079
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: ASCII(t
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/356,060A FILING DATE: 14-DEC-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 60 St
CITY: Boston
                                                                                                                                                   NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
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GCCCAGGGCACCATCCTCATCAACCGGGTGTTGGCCTCCTGCTACGCCGTCATCGAGGAG 1074
                                                                                                                                                                                                                                                                                                                                                                                                          CGGGAACTGCACCGCGGAGACTGGGTTTTTGGCGGCCGATGCGTCAGGCCGGGTGGTGCCC 708
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                                                                                                                                                                                                                                                                                                                                                                           GGCGGCTGCTTTCCGGGAAATGCAACTGTGCGCCTGTGGAGCGGCGAGCGGAAAGGGCTG
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                             GCGCACGGGACGCTGCTGGTGAACGATGTCCTGGCCTCTTGCTACGCGGTTCTGGAGAGT 1047
                                                           GCGTCTGTCCACAGCGTCTCATTGCGGGAGGAGGCGTCCGGAGCCTACGCCCCACTCACC
                                                                                        GCGCGCGTGGCCCGTGTGGC---GCGGGAGGAAGCCGTGGGGCGTGTTCGCGCCGCTCACC 987
                                                                                                                         CCCCAGCACCAGCCGGGGGCCACCAGGGGTCCACCAGTGGCCAGGCGCTCTTCGCCAGC
                                                                                                                                                                                                                     CGAGGGCCGCCCCCCCCCAGGCG-ACTTTGCACCGGTGTTCGCGCGCC----- 877
                                                                                                                                                                                                                                                  GAGACGCGGCAGCCCCGGGCCCGGCTGCTACTGACGGCGGCCCACCTGCTCTTTGTGGCC 834
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Pred. No. 1e-71;
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US-08-176-427B-5
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US-08-176-427B-5
                                                                                                                                                      Query Match
Best Local Similarity
Matches 552; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 57895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC COMPATIBLE
COMPUTER: IDM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CILASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REFERENCE/DOCKET NUMBER: HMI-006
REFERENCE/DOCKET NUMBER: HMI-006
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: McMahon, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1056 base pairs
TYPE: nucleic acid
STRANDENNESS: both
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                                                                                                  214 GAGCGCTTCCGGGACCTCGTGCCCAACTACAACCCCGACATCATCTTCAAGGATGAGGAG 273
                   274 AACAGTGGAGCCGACCCTGATGACCGAGCGTTGCAAGGAGAGGGTGAACGCTTTGGCC 333
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 60 St
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTCGGCTCCTACCGCTTAGCGGAGGAGCTACTGG 1186
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 AACACGGGTGCCGACCGCCTCATGACCCCAGCGCTGCAAGGACCGTCTGAACTCACTGGCC
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                                                                             GAGCGCTTCAAAGAGCTCACCCCCAACTACAATCCCGACATCATCTTCAAGGACGAGGAG
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                                                                                                                                                                       29.9%;
                                                                                                                                                    Score 355.8; DB 2; pred. No. 2.2e-66; 0; Mismatches 327;
                                                                                                                                                                                       Length
                                                                                                                                                        Indels
                                                                                                                                                                                             1056;
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RESULT 12
US-08-356-060A-3
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APPLICANT: Ingham,
                                                                                                                                                                                                           TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                               APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.
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STREET:
STRY: Boston
MA
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                                              COUNTRY: U. ZIP: 02109
                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGCTCAGTTGGCCTTCTGGCCCCTGCGACTGTTTCCC
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                                                                                                                                          60 State Street
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REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HNI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1056 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.9%;
Best Local Similarity 62.8%;
Matches 552; Conservative
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APPLICATION NUMBER: US 0
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 GAGCGCTTCCGGGACCTCGTGCCCAACTACAACCCCGACATCATCTTCAAGGATGAGGAG
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LOCATION:
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
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TOPOLOGY: Li
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    GCTTTCCAGGTCATCGAGACTCAGGATCCTCCGCGTCGGCTGGCGCTCACGCCTGCCCAC
                                           TCATTTGTGGCTGTGGAGACCGAGTGGCCTCCACGCAAACTGTTGCTCACGCCCTGGCAC
                                                                                                                    GCCCGGGTGGTGCCCACGCCGGTGCTGCTTCCTTGCACCGGGACTTGCAGCGCCGGGCT 753
                                                                                                                                                                                     GAGCGTGTGGCCCTGTCAGCTGTAAAGCCAGGAGACCGGGTGCTGGCCATGGGGGAGGAT
                                                                                                                                                                                                                                 GAGCGGAAAGGGCTGCGGGAACTGCACCGCGGAGACTGGGTTTTGGCGGCCCGATGCGTCA 693
                                                                                                                                                                                                                                                                               GCCGCTGCCAAGACAGGTGGCTGCTTTCCTGCCGGAGCCCAGGTGCGCCTAGAGAACGGG
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                                                                                            GGGACCCCCACCTTCAGTGATGTGCTTATTTTCCTGGACCGCGAGCCAAACCGGCTGAGA
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Pred. No. 2.2e-66;
"" ematches 327;
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Indels Length 1056;

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Gaps

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RESULT 13
US-08-356-060A-7
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                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/3
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/1
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATTHEW 1.56 700
                                                                                                                                                     TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.
                                         FEATURE:
                                                          MOLECULE TYPE:
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CITY: Boston
STATE: MA
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                    NAME/KEY:
                                                                                TOPOLOGY: 11
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ZIP: 02109
                                                                                                                                        ENGTH:
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Query Match

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Length 939;

US-08-176-427B-9

Sequence 9, Application US/08176427B Patent No. 5789543 GENERAL INFORMATION:

APPLICANT:
APPLICANT:

CANT: Ingham, Phillip W.
CANT: McMahon, Andrew P.
CANT: Tabin, Clifford J.
OF INVENTION: Vertebrate

Embryonic Pattern-Inducing

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                   1129 CCGACTGGCATGCATTGGTACTCTCGGCTCCTCTACCGCTTAGCGGAGGAGCTACTGG 1186
                                                                                                                                                                                               1009 AACGAIGICCIGGCCICTIGCIACGCGGITCCIGGAGAGICACCAGIGGGCGCACCGCGCT 1068
835 GGGGAGGGTGTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGGCGTCTCCTGCTAG
                                                                                                                                                                  724 GAGGATGTGGTGGCATCCTGCTTCGCGGCCGTGGCTGACCACCACCTGGCTCAGTTGGCC
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                                                                                                                           TTTGCCCCCTTGAGACTGCTGCACGCGCTAGGGGCGCTGCTCCCCGGCGGGGCCGTCCAG 1128
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                                                                                   TTCTGGCCCCTGAGACTCTTTCACAGCTTGGCATGG
                                                                                                                                                                                                                                                        TCTACACACGTGGCCCTCGGGGCCTACGCCCCCCCTCACAAAGCATGGGACACTGGTGGTG
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0; Mismatches 334;
                                                                                 -GGCAGCTGGACCCCG
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US-08-176-427B-9
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Best Local Similarity 58.4%;
Matches 571; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURENT APPLICATION DATA:
APPLICATION ASS
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Proteins and MUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,709 REFERENCE/DOCKET NUMBER: HM. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1256 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                            AAGTATGGGTTGCTGGCGCGCCTCGCAGTGGAAGCCGGCTTCGACTGGGTCTACTACGAG 531
                                                                                                                                                                                                                   GATTCACTCCACTACGAAGGCCGTGCTTTGGACATCACTACGTCTGACCGCGACCGCAAC 471
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                                                                                                                                                                                          GAATCACTCCACTACGAGGGAAGAGCTGTTGATATTACCACCTCTGACCGAGACAAGAGC
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                  TCCAAAGCCCACATTCATTGCTCTGTCAAAGCAGAAAATTCGGTTGCTGCGAAATCTGGG
                                                           AAATACGGGACACTGTCTCGCCTAGCTGTGGAGGCTGGATTTGACTGGGTCTATTACGAG
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Pred. No. 4.1e-58;
0; Mismatches 403;
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US-08-356-060A-5
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APPLICATION UNBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5844079
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5,
                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
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APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: LABLIC Street
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ZIP: 02109
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Best Local Similarity 58.4%;
Matches 571; Conservative
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TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1256 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                     GACTCGGTGCTGGCGCCC---GGGATGCGCCTTCGGCCAGCGCGCGTGGCCCGTGTG
                                                                                                                                    GAACTGCACCGCGAGACTGGGTTTTGGCGGCCGATGCGTCAGGCCGGGTGGTGCCCACG 711
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                                      AACTCAACGGAAGATCTCCACACCATGACCGCCGCGTATGCCAGCAGTGTCAGAGCCGGA 888
                                                                                                                                                                                                                                                              GGCTGCTTTCCGGGAAATGCAACTGTGCGCCTGTGGAGCGGCGAGCGGAAAGGGCTGCGG
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                                                               GGGCCGGCCCCCCCCAGGCGACTTTGCACCGGTGTTCGCGCGCCGGCTACGCGCTGGG
                                                                                      ACGCAAGAACCCGTTGAAAAGATCACCCTCACCGCCGCTCACCTCTTTTTGTCCTCGAC
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                                                                                                                                                                                      GACCTGAACCCCGGAGACAAGGTGCTGGCGGCAGACAGCGCGGGAAACCTGGTGTTCAGC
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Search completed: June 5, 2000, 07:57:16
Job time: 3807 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

Title:

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<b>4</b>	the treatment of parkinson's disease Disclosure; Page 97-99; 138pp; English. This nuclectide sequence comprises a coding region for the Dhh Desert hedgehog protein (see W97764). The invention is the finding that hedgehog proteins are useful as protective in the treatment and prophylaxis of neurodegenerative discoversulting from the loss of dopaminergic and/or GABA-nergic or the general loss of tissue from the substantia nigra. Exemplary discorders include Parkinson's disease, Huntington disease (both claimed), amyotrophic lateral sclerosis and ischaemia. The invention relates to hedgehog therapeutics hedgehog polypeptides and gene therapy constructs e.g. convenceding recombinant hedgehog polypeptides and trans-active constructs for altering hedgehog gene regulatory sequences to therapeutics (i.e. agents which mimic the effect of na curring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. A bloactive polypeptide comprising amino acid residues 23-198 of human preferrred. The products can also be used for the mainten of such neuronal cells in an animal. They can also be use prevent or treat neurodegenerative conditions arising from of certain drugs, and in the prevention and/or treatment on e.g. as a neuroprotective agent.  176 A; 375 C; 424 G; 215 T	170; 70; 70; 70; 70 st 70; 71 des 71; 71 des 71 de	33333333333333333333333333333333333333
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CAGAGCTGCGGGCCGGGGGGGGGCGGTTGGCCGGCGCTATGCGCGCAAGCAGCTC

ATGCCTCTCCTGACCAATCTACTGCCCTTGTGCTGCTTGCCACTTCTGGCGCTTGCCAGCC

ATGGCTCTCCTGACCAATCTACTGCCCTTGTGCTGCTTGGCCACTTCTGGCGCTGCCAGCC

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GTGCCGCTACTCTACAAGCAATTTGTGCCCGGCGTGCCAGAGCGGACCCTGGGCGCCAGT

GTGCCGCTACTCTACAAGCAATTTGTGCCCGGCGTGCCAGAGCGGACCCTGGGCGCCAGT

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PT A new method to regulate muscle growth
PT A new method to regulate muscle growth
PC Disclosure; Page 106-108; 130pp; English,
PC This nucleotide sequence comprises a coding region for the human
PC Desert hedgehog protein Dhh (see V05517). The invention relates to
PC this nucleotide sequence comprises a coding region for the human
PC Desert hedgehog protein Dhh (see V05517). The invention relates to
PC this nucleotide sequence of the formation and/or maintenance of muscle
PC this nucleotide is a method for modulating the formation and/or maintenance of muscle
PC the stamprogenitor cells, in vitro or in vivo, with a hedgehog
PC therapeutic (i.e. hedgehog polypeptides and gene therapy
PC constructs) or ptc therapeutic (i.e. a small organic molecule that
PC minics the effect of hedgehog proteins on patched signalling, or
PC constructs or potentiates patched signalling) in an amount effective
PC to alter the growth state of the treated cells. Also claimed is a
PC commetic repair of, such muscle tissues, by administering a
PC commetic repair of, such muscle tissues, by administering a
PC muscle atrophy, in particular skeletal muscle atrophy or cardiac
PC muscle atrophy, cachexia, or muscular myopathy (all claimed). The
PC myoblastic growth of muscle tissue such as in myoblastic or
PC myoblastic growth of muscle tissue such as in myoblastic sarcoma
PC (also claimed). The hedgehog therapeutic preferably comprises at
PC (also claimed). The hedgehog therapeutic preferably comprises at
PC (also claimed). The hedgehog gene (see X25098-107),
PC especially a human hedgehog gene.
PC (also PC) and provide treatment of a protein (see
PC) Sequence 1190 BP; 176 A; 375 C; 424 G; 215 T;
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Query Match
Best Local Similarity
Matches 1190; Conserv
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28-AUG_1998; JU17922.
29-AUG_1397; US-057394.
(ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1141
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Desert hedgehog; Dhh gene; human; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle a
cachexia; muscular myopathy; myoblastic sarcoma; therap
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X25105;
05-JUL-1999 (first
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Score 1190; DB 1;
; Pred. No. 1.4e-238;
0; Mismatches 0;
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                                          Length 1190;
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Desert hedgehog;
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                                 Homo sapiens
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                                                          (first entry)
                                       hedgehog protein o
nog; HuDHH; human;
/*tag=
67. .59
                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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14-apr-1998; JP-117873.

25-apr-1997; JP-121578.

(HAYB ) HAYASHIBARA SEIBUTSU K.
Ariyasu T, Nakamura S, Orita K
WPI; 98-544642/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody
Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Desert hedgehog protein - and corresponding
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28-OCT-1998:
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                                                                                                                         GTGCGCCTACGAGTGACTGAGGGCTGGGACGACGACGACCACGCTCAGGATTCACTC
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                                                         CACTACGAAGGCCGTGCTTTGGACATCACTACGTCTGACCGCGACCGCAACAAGTATGGG
                                                                                                           GTGCGCCTACGAGTGACTGAGGGCTGGGGACGACGACGCCACCACGCTCAGGATTCACTC
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14-APR-1998; JP-117873.

25-APR-1997; JP-111578.

(HAYB) HAYASHIBARA SEIBUTSU K
Ariyasu T, Nakamura S, Orita K
WPI; 98-544642/47.

P-PSDB; W79594.
antibody Claim 9; Page 22-23; 39pp; English.
Claim 9; Page 22-23; 39pp; English.
This cDNA sequence codes for a precursor (see W79594) of a novel human Desert hedgehog protein (see also W79593). Human Desert hedgehog protein DNA (HuDHH) was originally identified following screenings of human cell lines by PCR using primers (see V62402-03)
                                                             antibody
Claim 9;
                                                                                                                                                                                                                                    02-FEB-1999 (first entry)
Human Desert hedgehog protein
Desert hedgehog; HuDHH; human;
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V62394;
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indicated that the ARH-77 (ATCC CRL-1621) cell line, which is derived from the plasma cell of a leukammia patient, expressed a specific gene at an elevated level. Sequencing confirmed it to be a novel human gene showing homology to the mouse Desert hedgehog gene. DNA encoding C-terminal sequences (see V62398) was obtained by further PCR amplifications (see V62407-08). The invention provides Desert hedgehog polynucleotides and protein, a monoclonal antibody (MAD) that recognises the protein, a process for producing the protein, and a method for detecting the protein using the MAD. The hedgehog protein, DNA and MAD can be used to elucidate hereditary morphological abnormalities in humans to establish their treatments and diagnoses.
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Pred. No. 1.7e-222;
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                                                                                                PS Disclosure; Page 94-95; 130pp; English.

CC This nucleotide sequence comprises a coding region for the mouse CC Desert hedgehog protein Dhh (see Y05511). The invention relates to CC a method for modulating the formation and/or maintenance of muscle CC tissue by ecotopically contacting muscle cells, especially muscle CC stem/progenitor cells, in vitro or in vivo, with a hedgehog CC therapeutic (i.e. hedgehog polypeptides and gene therapy CC constructs) or ptc therapeutic (i.e. a small organic molecule that CC mimics the effect of hedgehog proteins on patched signalling, or CC constructs or potentiates patched signalling) in an amount effective to alter the growth state of the treated cells. Also claimed is a CC method for treatment or prevention of disorders of, or surgical or CC cosmetic repair of, such muscle tissues; by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be CC muscle atrophy, cachexia, or muscular myopathy (all claimed). The composition of polypeptide or ptc therapeutic can inhibit growth of medgehog polypeptide or ptc therapeutic can inhibit growth of compoblastic carowth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at CC (also claimed). The hedgehog therapeutic preferably comprises at CC (also claimed). The hedgehog therapeutic preferably comprises at CC (constitute extracellular portion of a hedgehog protein (see CC 905510-91) encoded by a vertebrate hedgehog gene (see X25098-107), CC especially a human hedgehog gene.

371 C; 399 G; 226 T;
                              Query Match
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Bladden CS, Currie PD, Hughes
WPI, 99-24355//20.
P-PSDB; Y05511.
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28-AUG-1998:--017922.
29-AUG-1997; US-057394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse Desert hedgehog protein Dhh cDNA.

Desert hedgehog; Dhh gene; mouse; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy; ds.
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Claim 5; Page 135-37; 210pp; English.

Claim 5; Page 135-37; 210pp; English.

The sequence encodes a mouse desert hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and has been isolated by construction of a mouse genome DNA library, in phage laws stringency screening of a mouse genome DNA library, in phage clambda. The sequence contains 3 homologous regions, encoding a clambda. The sequence contains 3 homologous regions, encoding a clambda. The sequence contains 3 homologous regions, encoding a clambda. The sequence contains a homologous regions, encoding a clambda. The sequence contains a splicing has compared to polymerase chain reaction amplification of first strand cDNA generated from adult testicle RNA. Probes and primers derived from hedgehog sequences may be used as diagnostic agents.

Control of the gene may also be used in gene therapy. Antibodies generated from the encoded protein may be used as therapeutic or research reagents.

So Sequence 1190 Bp; 194 A; 371 C; 399 G; 226 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 81.2%;
Best Local Similarity 88.3%;
Matches 1051; Conservative
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13-JUL-1995:
30-DEC-1994: U14992:
30-DEC-1993: US-176427:
14-DEC-1994: US-356060:
(HARD) HARVARD COLLEGE:
(IMCR) JUPPERLAL CANCER RES TINGHAM PW, MCMAhon AP, TAbii
WPI: 95-255060/33:
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Mouse; desert hedgehog gene; probe; primer;
nervous system disorder; gene therapy; antif
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X16183 stand X16183; 29-APR-1999

(first entry) CDNA;

standard;

ВP

Mouse Dhh hedgehog cDNA sequence.

Patched; hedgehog; ptc therapeutic; neuroprotective; neuron brain infarction; cerebral infarction; transient ischaemic stroke; cerebral infarct volume; spinal cord; oedema; traum

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DR P-SDB; W94469.

Proditions - is used for the treatment and prevention of e.g. conditions - is used for the treatment and prevention of e.g. corebral infarction, stroke and transient ischaemic attacks bisclosure; Page 65-66; 104pp; English.

Proditions - page 65-66; 104pp; English.

CA method has been developed for limiting the damage to neuronal cells by ischaemic or epoxic conditions by administering a ptc (patched) therapeutic agent to reduce cerebral infarct volume (CIV). Damage to construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this corebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic attacks. It may also be used as a prophylactic in many other cases of conjury to the brain or spinal cord, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The treatment reduces CIV by at least 25, particularly at least 70,%. The
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07-JAN-1999.
26-JUN-1998; U13387.
27-JUN-1997; US-883656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence encodes a hedgehog sequence given in the present invention.
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WPI; 99-095458/08.
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/note= "no stop codon given"
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                                   (ONTO-) ONTOGENY INC.
Mahanthappa NK, Miao N
WPI; 99-142578/12.
P-PSDB; W97766.
                                                                                                                                                                                                              Mouse Desert hedgehog (Dhh) cDNA.

Desert hedgehog; Dhh gene; mouse; dopaminergic; GABA-nergic ptc therapeutic; patched; signal transduction; Parkinson's Huntington's disease; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1081
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04-FEB-1999.
24-JUL-1998; U15419.
24-JUL-1997; US-900220.
Increasing the survival cells - by using a ptc 1
                                                                                                                                                                                                   cerebral
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21-MAY-1999
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Disclosure; Page 85-86; 138pp; English.

CC This nuclectide sequence comprises a coding region for the mouse comprises are useful as protective agents code the finding that hedgehog proteins are useful as protective agents code the finding that hedgehog proteins are useful as protective agents code the finding that hedgehog proteins are useful as protective agents code the finding that hedgehog proteins are useful as protective agents code the finding that hedgehog proteins are useful as protective disorders.

CC resulting from the loss of dispaminergic and/or GABA-nergic neurons, code the general loss of tissue from the substantia nigra.

CC exemplary disorders include parkinson's disease, Huntington's disease (both claimed), amyotrophic lateral scherosis and cerebral code is chamber to hedgehog polypeptides and trans-activation code neoding recombinant hedgehog polypeptides and trans-activation constructs for altering hedgehog polypeptides and trans-activation constructs for altering hedgehog polypeptides and trans-activation coccurring hedgehog proteins on patched signalling) that are coccurring hedgehog proteins on patched signalling) that are coccurring hedgehog proteins on patched signalling) that are coccurring hedgehog proteins on patched signalling in an also be used for the maintenance of differentiated neurons in cultures, can discobe used for the maintenance of differentiated neurons in cultures, can discobe used for the maintenance of differentiated neurons and in the coccurring hedgehog polypeptides and seed to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the conditions arising from the use of certain drugs, and in the coccurring hedgehog polypeptides and to enhance the implantation of such neurons in cultures, and the pro
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Pred. No. 1.8e-192;
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                                          CCCGCGCCAGGCGACTTTGCACCGGTGTTTCGCGCGCCGGCTACGCGCTGGGGACTCGGTG
                                                                                    GCCTCCTGCTACGCGGTTCTAGAGAGTCACCAGTGGGCCCACCGCGCCTTCGCCCCTTTG
                                                                                                GCCTCTTGCTACGCGGTTCTGGAGAGTCACCAGTGGGCGCACCGCGCTTTTTGCCCCCCTTG
                                                                                                                                       GCCGTGGGCGTGTTCGCGCCGCTCACCGCGCACGGGACGCTGCTGGTGAACGATGTCCTG
                                                                                                                                                                                   CTGGCGCCCGGCGGATGCGCCTTCGGCCAGCGCGTGGCCCCTGTGTGGCGCGGGAGGAA
                                                                                                                                                                                                                                                                     CCTCCACGCAAACTGTTGCTCACGCCCTGGCACCTGGTGTTTGCCGCTCGAGGGCCGCG
                                                                                                                                                                                                                                                                                                                CTCTTCCTGGACCGGGACTTGCAGCGCCGGGCTTCATTTGTGGCTGTGGAGACCCGAGTGG
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                                                                                                                                                                                                                                                            CCTCCGCGCAAACTGTTGCTCACACCCTGGCATCTGGTGTTCGCTGCTCGCGGGCCAGCG
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                                                                                                                               GCCGTGGGCGTGTTCGCACCGCTCACTGCGCACGGGACGCTGCTGGTCAACGACGTCCTC
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RESULT
V62397
         antibody

Example 1-2; Page 27-28; 39pp; English.

This cDNA sequence codes for the N-terminal region (see W79597) of a precursor form (see W79595) of novel human Desert hedgehog protein (see also W79593). Human Desert hedgehog protein DNA (HuDHH) was originally identified in human following ARH-77 (ATCC CRL-1621) cell line following ART-PCR amplification screenings. Further PCR (see V62405-06) yielded cDNA encoding the N-terminal region. DNA molecules (see V62393-95) encoding mature and precursor forms (see W79593-95) of human Desert hedgehog are claimed, as are a monoclonal
                                                                                                                                                                                                      28-OCT-1998.
24-APR-1998;
14-APR-1998;
25-APR-1997;
                                                                                                                                                    (HAYB) HAYASHIBARA SEIBUTSU
Ariyasu T. Nakamura S. Orita
WPI: 98-544642/47.
P-PSDB; W79597.
                                                                                                                                                                                                                                                                                                                                                  Human Desert hedge Desert hedgehog;
                                                                                                                                                                                                                                                                                                                                                                                        V62397;
                                                                                                                                      Human Desert hedgehog
                                                                                                                                                                                                                                                           EP-874048-A2.
                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                      303187.
JP-117873.
JP-121578.
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                hedgehog
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/*tag= a
73. .600
/*tag= b
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  gehog protein N-terminal HuDHH; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                      CDNA; 602
                                                                                                                                      protein -
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                                                                                                                                      and
                                                                                                                                      corresponding DNA and
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Best Local S
Matches 590
 28-OCT-1998.
24-APR-1998; 303187.
24-APR-1998; JP-117873.
14-APR-1997; JP-121578.
25-APR-1997; JP-121578.
(HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
Ariyasu T, Wakamura S, Orita K;
WPI; 98-546042/47.
P-PSDB; W79598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody (MAb) that recognises the protein, a process for producing the protein, and a method for detecting the protein using the MAb. The hedgehog protein, DNA and MAb can be used to elucidate hereditary morphological abnormalities in humans to establish their treatments and diagnoses.

Sequence 602 BP; 111 A; 187 C; 199 G; 105 T;
                                                                                                                                                             V62398;
V62398;
                                                                                                                               Human Desert hedo
Desert hedgehog;
                                                                                                    mat_peptide
                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                       CACGTCCACGTGTCGGTCAAAGCTGATAACTCACTGGCGGTCCGGGCGGCGGCTG
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                                                                                                                                                                                                                                                                                                                CACTACGAAGGCCGTGCTTTGGACATCACTACGTCTGACCGCGACCGCAACAAGTATGGG
                                                                                                                                                                                                                                                                                                                                                        GTGCGCCTACGAGTGACTGAGGGCTGGGACGAGGACGGCCACCACGCTCAGGATTCACTC
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                                                                                                                                                                       standard; cDNA; 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                             (first entry)
: hedgehog protein C-terminal region
:hog; HuDHH; human; ds.
                                                                                                  Location/Qualifiers
2..574
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99.0%;
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Pred. No. 1.7e-113;
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This cDNA sequence codes for the C-terminal region (see W79598) of a precursor form (see W79594) of novel human Desert hedgehog protein (see also W79593). Human Desert hedgehog protein DNA (HuDHH) was criginally identified in human following RH-77 (ATCC CRL-1621) cell line following RT-PCR amplification screenings. Further PCR (see V62407-08) yielded cDNA encoding the C-terminal region. DNA molecules (see V62393-95) encoding mature and precursor forms (see W79593-95) of human Desert hedgehog are claimed, as are a monoclonal antibody (MAb) that recognises the protein, a process for producing the protein, and a method for detecting the protein using the MAb. The hedgehog protein, DNA and MAb can be used to elucidate treatments and diagnoses.

Sequence 575 BP; 66 A; 183 C; 221 G; 105 T;
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Best Local Similarity 99.8
Matches 574; Conservative
                    v62396 standard; cDNA; 548 BP.
v62396; 02-FEB-1999 (first entry)
Human Desert hedgehog protein of Desert hedgehog; HuDHH; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCACGCGCTAGGGGCCCTGCTCCCCGGCGGGGCCG
                                                                                                                                                                                                                             CTACGCGGTTCTGGAGAGTCACCAGTGGGCGCACCGCGCTTTTGCCCCCCTTGAGACTGCT
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                                                                                                                                                        GCACGCGCTAGGGGCGCCTCCCCCGGCGGGGCCG
                                                                                                                                                                                                                                                                       CGTGTTCGCGCCGCTCACCGCGCACGGGACGCTGCTGGTGAACGATGTCCTGGCCTCTTG
                                                                                                                                                                                                                                                                                      CGTGTTCGCGCCGCTCACCGCGCACGGGACGCTGGTGAACGATGTCCTGGCCTCTTG
                                                                                                                                                                                                                                                                                                                               CGGCGGGATGCGCTTCGGCCAGCGCGCGTGGGCCCGTGTGGCGCGGGAGGAAGCCGTGGG
                                                                                                                                                                                                                                                                                                                                            TGCAACTGTGCGCCTGTGGAGCGGCGAGCGGAAAGGGCTGCGGGGAACTGCACCGCGGAGA
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Pred. No. 8.2e
0; Mismatches
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Homo sapiens. Key

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CDNA clone pHuDHH/#20 codes for a precursor (see W79596) of novel thuman Desert hedgehog protein (see also W79593). Human Desert hedgehog protein see also W79593). Human Desert hedgehog protein DNA (HuDHH) was originally identified following extensive screenings of human cell lines by PCR using primers (see V62402-03) based on the mouse Desert hedgehog gene. These screenings indicated that the ARH-77 (ATCC CRL-1621) cell line, which is derived from the plasma cell of a leukaemia patient, expressed a specific gene at an elevated level. Sequencing confirmed it to be a novel human gene showing homology to the mouse Desert hedgehog gene. Nucleotide sequences (see W62393-95) encoding mature and precursor forms (see W79593-95) of human Desert hedgehog are claimed, as are a monoclonal antibody (MAb) that method for detecting the protein using the MAB. The hedgehog protein, DNA and MAB can be used to eludate hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
Ariyasu T, Nakamura S, Orita K;
WPI; 98-544642/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1998.
24-APR-1998; 303187.
24-APR-1998; JP-117873.
25-APR-1997; JP-121578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  morphological abnormalities in humans to establish their treatments and diagnoses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Desert hedgehog protein - and corresponding
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                                                                                                    CAGGATTCACTCCACTACGAAGGCCGTGCTTTGGACATCACTACGTCTGACCGCGACCGC
                                                                                                                                                                                                     CTCGTGCCCAACTACAACCCCGACATCATCTTCAAGGATGAGGAGAACAGTGGAGCCGAC
                                                                                                                                                                                                                                                                                                                                                                            CGCAAGCAGCTCGTGCCGCTACTCTACAAGCAATTTGTGCCCGGCGTGCCAGAGCGGACCC
GAGTCCCGCAACCACGTCCACGTGTCGGTCAAAGCTGATAACTCACTGGCGGTCCGGGCG
                                             AACAAGTATGGGTTGCTGGCGCGCCTCGCAGTGGAAGCCGGCTTCGACTGGGTCTACTAC
                                                                                     CAGGATTCACTCCACTACGAAGGCCGTGCTTTGGACATCACTACGTCTGACCGCGACCGC
                                                                                                                                                             ATGTGGCCCGGAGTGCGCCTACGAGTGACTGAGGGCTGGGACGACGACGACGGCCACGCT
                                                                                                                                                                                                                                                                           CTCGTGCCCAACTACAACCCCGACATCATCTTCAAGGATGAGGAGAACAGTGGAGCCGAC
                                                                                                                                                                                                                                                                                                                     CTGGGCGCCAGTGGGCCAGCGGAGGGGAGGGTGGCAAGGGGCTCCGAGCGCTTCCGGGAC
                                                                                                                                             ATGTGGCCCGGAGTGCCCCTACGAGTGACTGAGGGCTGGGACGACGACGGCCACCACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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/*tag= a
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 540; DB 1; Pred. No. 6.8e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be a novel human gene showing homology to the mouse Desert hedgehog gene. Nucleotide sequences (see V62394 95) encoding precursor forms (see W79594-95) of human Desert hedgehog are also claimed, as are a monoclonal antibody (MAb) that recognises the protein, as process for producing the protein, and a method for detecting the protein using the MAb. The hedgehog protein, DNA and MAb can be used to elucidate hereditary morphological abnormalities in humans to establish their treatments and diagnoses.

Sequence 528 BP; 101 A; 160 C; 181 G; 86 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This cDNA sequence codes for novel human Desert hedgehog protein mature polypeptide (see W79593). Human Desert hedgehog protein DNA (HADHH) was originally identified following extensive screenings of human cell lines by PCR using primers (see V62402-03) based on the mouse Desert hedgehog gene. These screenings indicated that the ARH-77 (ATCC CRL-1621) cell line, which is derived from the plasma cell of a leukaemia patient, expressed a specific gene at an elevated level. Sequencing confirmed it to be a novel human gene ehvated level.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody Claim 8; Page 20-21; 39pp; English.
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24-APR-1998; 303187.
14-APR-1998; JP-117873.
25-APR-1997; JP-121578.
(HAYB ) HAYASHIBARA SEIBUTSU
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02-FEB-1999
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                                                      TGCAAGGAGAGGGTGAACGCTTTGGCCATTGCCGTGATGAACATGTGGCCCCGGAGTGCGC
                                                                                                               CCCGACATCATCTTCAAGGATGAGGAGAACAGTGGAGCCGACCGCCTGATGACCGAACGT
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DR PPSDB; W94474.

PT Method for limiting damage to neurons caused by ischaemic or epoxic PT conditions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks

PT cerebral infarction, stroke and transient ischaemic attacks

PS Disclosure; Page 74.76; 104pp; English.

CC A method has been developed for limiting the damage to neuronal cells by CC ischaemic or epoxic conditions by administering a ptc (patched) concurronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a construct which recombines with the genomic hedgehog gene to provide a crebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic or ischaemic crebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic can attacks. It may also be used as a prophylactic in many other cases of conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The treatment reduces CIV by at least 25, particularly at least 70.8. The
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X16188;
29-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9900117-A2.
07-JAN-1999.
26-JUN-1998; U13387.
27-JUN-1997; US-883656.
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WPI; 99-095458/08.
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                                GGGCCGTCCAGCCGACTGGCATTGGATTGGTACTCTCGGCTCCTCTACCGCTTAGCGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PT increasing the survival of neuronal, dopaminergic and GABA-nergic recils - by using a ptc therapeutic such as a protein kinase rinhibitor, or an agent derived from hedgehog polypeptides, useful in the treatment of Parkinson's disease ps Disclosure; Page 95-97; 138pp; English.

CC This nucleotide sequence comprises a coding region for the human CC Inhi Indian hedgehog protein (see W97763). The invention is based on the finding that hedgehog proteins are useful as protective agents CC in the finding that hedgehog proteins are useful as protective agents CC in the general loss of dopaminergic and/or GABA-nergic neurons, CC or the general loss of dopaminergic and/or GABA-nergic neurons, CC Exemplary disorders include parkinson's disease, Huntington's CC include parkinson's disease, Huntington's CC include parkinson's disease, Huntington's CC include parkinson's clarosis and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. agents which mimic the regulatory sequences) and ptc hedgehog polypeptides and trans-activation cc constructs for altering hedgehog yolypeptides and trans-activation occurring hedgehog proteins on patched signaling) that are effective in both human and animal subjects. A bloactive proferried. The products can also be used for the maintenance of clifferantiated neurons in cultures, and to enhance the implantation of preferried. The products can also be used for the maintenance of constructs and animal and animal. They can also be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the prevention and/or treatment of hypoxia, e.g. as a neuroprotective agent.

Sequence 1622 BP; 277 A; 549 C; 510 G; 286 T;
                                                                                                                                                                                                                                                                                                                                                                        Matches
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Mahanthappa NK, Miao N, Pang
WPI; 99-142578/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Problem of the regulate muscle growth problem of the human comprises a coding region for the human color indian hedgehog protein in his (see y05516). The invention relates to constant the color protein for maintenance of muscle color in the following muscle cells, especially muscle constructs or put the properties and gene therapy constructs or protein for the small organic molecule that constructs or protein for polypeptides and gene therapy constructs the effect of hedgehog proteins on patched signalling, or constructs or potentiates patched signalling in an amount effective to alter the growth state of the treated cells. Also claimed is a method for treatment or prevention of disorders of, or surgical or commetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be nedgehog polypeptide or ptc therapeutic atrophy or cardiac mysolastic growth of muscle tissue to provide treatment of hyperblastic or neoplastic growth of muscle tissue such as in mysolastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at constant a bioactive extracellular portion of a hedgehog protein (see cost). Sequence 1622 Bp; 277 A; 549 C; 510 G; 286 T;
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Matches 730
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04 MAR-1999
28-AUG-1998; U17922
29-AUG-1997; US-057394.
(ONTO-) ONTOGERY INC.
Bladgen CS, Currie PD, Hughes SI
WPT; 99-243557/20.
P-PSDB; Y05516.
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Human Indian hedgehog protein Ihh cDNA.

Indian hedgehog; Ihh gene; human; hedgehog therapeutic;

ptc therapeutic; patched; signal transduction; muscle atrophy;

cachexia; muscular myopathy; myoblastic sarcoma; therapy; ds.
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                                                 CCGTGATGAACATGTGGCCCGGAGTGCGCCTACGAGTGACTGAGGCCTGGGACGACGACGA
                                                                                                     GCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACA
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30; Conservative
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Pred. No. 5.4e-86;
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Search completed: June 5, 2000, 07:58:49 Job time: 3814 sec

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re greater than or equal to the score of the result being printed,
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Cell 75, 1417-1430, 1993
A:Title: Sonic hedgehog, a
A:Reference number: A49425
A:Accession: B49425
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849425

besert hedgehog protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C:Accession: B49425
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A;Molecule type: DNA
A;Residues: 1-396 <ECH>
A;Cross-references: GB:X76292; NID:g443941; PIDN:CAA53924.1; PID:g443942
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C:Superfamily: sonic hedgehog protein
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Scoring table:

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Post-processing: Minimum Match Listing first

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pir1:\*
pir2:\*
pir3:\*
pir4:\*

Title: Perfect score:

US-08-900-220-17 2088

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2000, 08:17:52;

protein -8::

protein search, using

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model

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RESULT 2
A49425
Sonic hedgehog protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Accession: A49425
R;Echelard, Y; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.;
Cell 75, 1417-1430, 1993
A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is i:
A;Reference number: A49425; MUID:94094334
A;Accession: A49425
A;Status: preliminary; nucleic acid sequence not shown
A;Mclecule type: mRNA
A;Residues: 1-437 <ECH>
A;Cross references: GB:X76290
A;Note: authors translation is shown for the codon TCC at position 436
C;Genetics:
A;Gene: Shh
C;Superfamily: sonic hedgehog protein
RESULT 3
B53193
hedgehog homolog vhh-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Apecies: Normania (Norway rat)
C;Apecies: Rattus norvegicus (Norway rat)
R;Reelink, H.; Augsburger, A.; Heemskerk, J.; Korzh, V.; Norlin, S.; Ruiz i Altaba, A.;
Cell 76, 761-775, 1994
A;Title: Floor plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgeh
A;Title: Floor plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgeh
A;Reference number: A53193; MUID:94170375
A;Rocession: B53193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-437 - ROE>
A;Cross-references: GB:L27340; NID:g452122; PIDN:AAA20999.1; PID:g452123
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Les 249; Conservative
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1.1e-89;
hes 82;
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C; Superfamily: sonic hedgehog protein
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C;Superfamily: sonic hedgehog protein
F;1-26/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-425 <RID>
                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: A49424
R;Riddle, R.D.; Johnson, R.L.; Laufer, E.; Tabin, Cell 75, 1401-1416, 1993
A;Title: Sonic hedgehog mediates the polarizing ac A;Reference number: A49424; MUID:94094333
A;Accession: A49424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patterning protein Sonic hedgehog precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
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Best Local Similarity
Matches 245; Conserv
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Best Local Similarity
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118 WPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYE 177
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                                                                              GASGPAEGRVARGSERFRDLVPNINPDIIFKDEENSGADRLMTERCKERVNALAIAVMMM 117
                                                                                                                                                                          MALLTNLLP---LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL 57
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                                                            GASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQ 119
                                                                                                                                       MLLLTRILLVGFIC -- ALLVSSGLTCGPGRG-IGKRRHPKK-LTPLAYKQFIPNVAEKTL 59
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57.8%;
                                                                                                                                                                                                                                      57.4%; Score 1198; DB 2; Length 425; 59.4%; Pred. No. 3.6e-88;
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Pred. No. 1.5e-88;
2; Mismatches 87;
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41;

Gaps

7;

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hedgehog homolog vhh-1 - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Species: Brachydanio rerio (zebra fish)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
C;Accession: A53193
R;Rocelink, H.; Augsburger, A.; Heemskerk, J.; Korzh, V.; Norlin, S.; Ruiz i Altaba, A.;
Cell 76, 761-775, 1994
A;Title: Floor plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgeh
A;Reference number: A53193; MUID:94170375
A;Accession: A53193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-418 <ROE>
A;Cross-references: GB:L27585; NID:9452159; PID:g452160
C;Superfamily: sonic hedgehog protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 WPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYE 179
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Local Similarity 54.3%;
nes 220; Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                  PLRLLHALGALL-----PGGAVQPTGMHWYSRLLYRLAEELL
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                                                                                                                                                                                                                                                                     AHIHCSVKAENSVAAKSGGCFPGSALVSLQDGGQKAVKDLNPGDKVLAADSAGNLVFSDF
                                                                                                                                                                                                                                                                                                                                                NHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QWAHRAFAPURLLHA-LGALLPGGAV-----QPTGMHWYSRLLYRLAEELL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFLTFLDRMDSSRKLFYVIETRQPRARLLLTAAHLLFVAPQHNQSEATGSTSGQALFASN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVLLFLDRDLQRRASFVAVETEWPPRKLLLIPWHLVFAA--RGPAPAPGDFA--PVFARR 293
                                                                                           PARLYYYVSSFLFPQNSSSRSNATLQQEGVHWYSRLLYQMGTWLL
                                                                                                                                                                      VMVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTIVVDRILASCYAVIEDQGLAHLAFA
                                                                                                                                                                                                                                               IMFTDRDSTTRRVFYVIETQEPVEKITLTAAHLLFVLDNSTEDLHTMTAAYASSVRAGQK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMNHWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MRLTRVLLVSLUTLSLVVSGLACGPGRG-YGRRRHPKK-LTPLAYKQFIPNVAEKTLGA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MALLTNLLPLCCLAL-LALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKAHIHCSVKAENSVAAKSGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYS
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precursor -
African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1120; DB 2;
Pred. No. 5.9e-82;
6; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                  395
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C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 10-Dec-1999
C;Accession: S56765
R;Stolow, M.A.; Shi, Y.B.
Nucleic Acids Res. 23, 2555-2562, 1995
A;Title: Xenopus sonic hedgehog as a potential morphogen during embryogenes
A;Reference number: S56765; MUID:95357169
A;Accession: S56765
                                                                                                                                                                R:Krauss, S.; Concordet, J.P.; Ingham, P.W. cell 75, 1431-1444, 1993
A:Title: A functionally conserved homolog of A;Reference number: A49426; MUID:94094335
A;Accession: A49426
                                                                                                                                                                                                                                                           sonic hedgehog gene shh protein - zebra fish R;Alternate names: local cell-cell interaction signaling protein C;Species: Brachydanio rerio (zebra fish) C;Date: 06-Oct-1994 *sequence_revision 18-Nov-1994 *text_change | C;Rccession: A49426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: I-444 <STO>
A; Cross references: EMBL:L39213; NID:C; Superfamily: sonic hedgehog protein
                                                   A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone
C:Superfamily: sonic hedgehog protein
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                                                                                                            A;Status: preliminary; not compared A;Molecule type: nucleic acid A;Residues: 1-415 <KRA>
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Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 TMTLKAVKVEKVDLEEDTGAYAPLTAHGTVVIDQVLASCYAVIEEHTWAHLAFAPLREGM 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVT 126
: | |: |::| |||||:||||:|||||:|||||
ITRNSDCFKELTPNYNPDIMFKDEESTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLSFIC-TLVTPPGLACGPGRG-IGKRRHPKK-LTPLAYKQFIPNVAEKTLGASGRYEGK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDVKKLFYVIETS--QRKIRLTAAHLLFVAQTKVNGTRSFKSVFASNIQPGDLIYTADPK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQRRASFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSVLA--PG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL:L39213; NID:g790937; PID:g790938
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51
. 28;
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Pred. No. 1e-79;
Score
                                                                                                                                                with
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1069;
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2;
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Length 415;
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segment

polarity

gene

424

364

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R:EChblard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J. Cell 75, 1417-1430, 1993
A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, A;Reference number: A49425; MUID:94094334
A;Accession: C49425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
C49425
Indian hedgehog protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: C49425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: X76291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-336 <ECH>
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Best Local S
Matches 190
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      241 RVAAVSTHVALGSYAPLTRHGTLVVEDVVASCFAAVADHHLAQLAFWPLRLFPSLAWGSW 300
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                                                                                                                                                                                                                                                                                                                                                                        NHVHVSVKADNSLAVRAGGCEPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPV 239
                                                      RVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLLHAL--GAL 369
                                                                                                                                                                                                                                                     AAAKTGGCFPAGAQVRLENGERVALSAVKPGDRVLAMGEDGTPTFSDVLIFLDREPNRLR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERFRDLVPNYNPDIIFKDEENSGADRIMTERCKERVNALAIAVMNMWPGVRLRVTEGWDE 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVRLRVTEGWDEDGHHADDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGEDWVYYESR 179
                                                                                                                            AFQVIETQDPPRRLALTPAHLLFIADNHTEPAAHFRATFASHVQPGQYVLVSGVPGLQPA 240
                                                                                                                                                                                      SFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSVLAPGGDALRPA 311
                                                                                                                                                                                                                                                                                                               LAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRDLQRRA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDRLNSLAISVMNQWPGVKLRVTEGRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHIHCSVKAENSVAAKSGGCFPGSALVSLQDGGQKAVKDLNPGDKVLAADSAGNLVFSDF 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VMVVDDSGQLKSVIVQRIYTEEQRGSFAPVTAHGTIVVDRILASCYAVIEDQGLAHLAFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNSLAISVMNHWP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 956.5;
Pred. No. 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.1e-69;
ches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9e-78;
ches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4,
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C;Species: Drosophila melanogaster
C;Date: 07-Apr-1994 #sequence_revision 18-NC
C;Accession: A46400; JN0501; A43480
R;Tabata, T.; Eaton, S.; Kornberg, T.B.
Genes Dev. 6, 2635-2645; 1992
A;Title: The Drosophila hedgehog gene is expanded to the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:LO5404
A;Note: It is uncertain whether Met-1 or Met-51 is the initiator A;Note: intron positions were determined from partial DNA sequence R;Lee, J.J.; von Kessler, D.P.; Parks, S.; Beachy, P.A.
Cell 71, 33-50, 1992
A;Title: Secretion and localized transcription suggest a role in pc A;Reference number: A43480
A;Accession: A43480
A;Status: preliminary; not compared with conceptual translation a.Mcleonia trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: FlyBase:FBgn0004644
A;Introns: 160/3; 248/1
C;Superfamily: sonic hedgehog protein
C;Keywords: transmembrane protein
F;62-82/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:S66384; NID:g435848; PID:g435849
A;Experimental source: Oregon-R
A;Note: sequence extracted from NCBI backbone (NCBIN:138996, NCBIP:138997)
R;Tashiro, S.; Michiue, T.; Higashijima, S.; Zenno, S.; Ishimaru, S.; Takahashi, F.;
Gene 124, 183-189, 1993
A;Title: Structure and expression of hedgehog, a Drosophila segment-polarity gene req
A;Reference number: JN0501; MUID:93185922
A;Accession: JN0501
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A;Note: sequence extracted from NCBI backbone (NCBIP:115418)
C:Comment: This protein is required for cell-cell communicat
C:Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-471 <TAS>
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A; Residues: 1-471 <TAB>
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Best Local
                                                                                                                                                                                                                                                     118
   238
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                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 49.4 nes 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               4 LINLLPLCCLALLAL-----PAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLG
RRHIYCSVKSDSSISSHVHGCFTPESTALLESGVRKPLGELSIGDRVLSMTANGQAVYSE
                                                                                                                                                            PGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYES 178
                                                                                                                                                                                                                                            RNHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTP
                                                                                                                                                                                                                                                                                                            ASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNÆLAIAVMNMW 118
                                                                                                                                                                                                                                                                                                                                                                        LSRLTSLVALLLIVLPMVFSPAHSCGPGRG-LGRHR--ARNLYPLVLKQTIPNLSEYTNS
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                                                                                                                            PGIRLLVTESWDEDYHHGQESLHYEGRAVTIATSDRDQSKYGMLARLAVEAGFDWVSYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 951; DB 2; 1
Pred. No. 2.1e-68;
0; Mismatches 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-J
C;Accession: G02735
R;Drummond, I.A.
submitted to the EMBL Data Library, June 19
A;Reference number: H01643
A;Recession: G02735
A;Status: preliminary; translated from GB/E
A;Molecule type: mRNA
A;Residues: 1-94 <DRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U59748; NID:g1401271; PID:g1401272 C;Genetics: A;Gene: hDHH
                                                                                                                                                                                                     A:Cross-references: EMBL: 281540; p
A:Experimental source: clone F46B3
C:Genetics:
A:Gene: CESP:F46B3.5
A:Map position: 5
A:Introns: 45/3; 200/1; 235/3; 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F46B3.5 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T22281 R;Ainscough, R.
                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A; Reference number: Z19541 A; Accession: T22281 A; Status: preliminary; translated fi
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A; Residues: 1-868 <W
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C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997
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Best Local S
Matches 93
                                                                                                                                                                                                  Map position: 5; Introns: 45/3; 200/1;
                                                                                                    Query Match
Best Local Similarity
Matches 63; Conserv
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                         662
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                                                 197 GGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVP--TPVLLFLDRDLQRRASFV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 IIFKDEENSGADRLMTERCKERVNALAIAVMNWPGVRLRVTEGWDEDGHHAQDSLHYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVLAPGGDA--LRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VILEMDRNLEQMQNFVQLHTD-GGAVLTVTPAHLVSVWQ---PESQKLTFVFADRIEEKN
                     GGCFSSDTLVTTPSG-KKRMDEIDVGDYVLTAN---RVKTHFTPVTLWIHRESEKLEEFL 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RALDITTSDRDRNKYGLLARLAVEAGFDWVYYGS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
                                                                                                                                                                                                                                                                                                                                 1-868 <WIL>
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                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                         EMBL: 251540; PIDN: CAB04405.1; GSPDB: GN00023;
                                                                                                                                                                                                         235/3; 436/3; 561/3; 581/3; 696/3; 742/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.7%;
                                                                                                                          10.0%;
                                                                                                  Score 209; DI; Pred. No. 7.5; 37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 495; DB 2;
Pred. No. 7.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                     November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GGAVQPTGMHWYSRLLYRLAEELL 395
                                                                                                                                                                                                                                                                                                                                                                         GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB/EMBL/DDBJ
                                                                                                    DB 2; 1
7.5e-09;
hes 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                      Length 868
                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                      24;
                                                                                                                                                                                                                                                                                                             CESP: F46B3.
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                                                                                                                                                                                                         826/3;
                                                                                                  Gaps
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                                                                                                                                                                                                         846/3
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                                                     A;Status: preliminary; translated from GB/EMBL/DDB
A;Molecule type: DNA
A;Residues: 1-1021 <WIL>
A;Cross references: EMBL:281560; PIDN:CAB04547.1;
A;Experimental source: clone K02E2
                                                                                                                                                            submitted to the EMBL Data A; Reference number: Z19716 A; Accession: T23252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1226 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein R08B4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                             hypothetical protein K02E2.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T23252
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A; Introns: 53/2; 113/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:268008; PIDN:CAA92000.1; GSPDB:GN00028; CESP:R08B4
A;Experimental source: clone R08B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: T24045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: R; White, S.
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                                                                                                                                                                                                                            R;Lloyd, C
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  A; Map
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Best Local S
Matches 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1012 SALVAATGACFSLDTWVTTPTG-KKRMDQIDIGDYVLTADLE-KTYFTPITLWIHREPEK 1069
                                                                                                                                                                                                                                                                                                                                                                                                                1189 LRSV-LVEFFGDLYNNKIELPTG 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1070 VQEFLTIMTEY-GKTLRITSRHFMYRNKCGKSYPQYIKMLPHDGEAIFASDLEVGDCVVV 1128
position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 NSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRDLQR 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          834 KVLNLFGILHMNEIELPTGTAVYKELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 -LLHALGALLPGGAVQPTGMHWYSRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 RASFVAVETEWPPRKLLLTPWHLVFAAR-GPA-----PAPGDFAPVFARRLRAGDSVLA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
                     CESP:K02E2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CESP: R08B4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAPLRLLHALGALLPGGAVQPTG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVETEWPPRKLLLTPWHLVFAARGPAPA-----PGDFAPVFARRLRAGDSVLAPGGDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLE-----SHQWAHRAFAPLR- 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITTE-RGSTLQLTPLHFMYRTKCNESSEFLKILPENHEAILASYLEIGDCVILTENTKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYKGKYRQQKIETITRSVRTGIYSPLTNNGRIIVNDMLASCYSEIQQNTLQTTFFWAYDK 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGGDALRPARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQ-----WAHRA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROEKINOTTRGLKTGIYSPLTKNGRIIVNDMLASCYSEVQANVLQTTYFW---VFNRLRQ 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152/3; 204/3; 272/1;
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                                                                                                                                                                                                     Library,
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Pred. No. 1.6e
44; Mismatches
                                                                                                                                           from GB/EMBL/DDBJ
                                                                                                                                                                                                     November 1996
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1.6e-07;
hes 87;
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                                                                               GSPDB:GN00023; CESP:K02E2.2
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877/1;

7;

A; Introns: 41/1; 79/3; 131/3; 197/1; 262/1; 297/3; 566/3; 610/3; 735/3; 775/3; 834/3;

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R:Thomas, K.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19793
A:Accession: T23754
A:Accession: T23754
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A; Residues: 1-1207 <WIZ>
A; Cross-references: EMBL: Z66500; PIDN: CAA91313.1; GSPDB: GN00020; CESP: T05C12.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, October 1995 A; Reference number: Z19901 A; Accession: T24513
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A;Residues: 1-1207 <WIL>
A;Cross-references: EMBL:249968; PIDN:CAA90265.1; GSPDB:GN00020; CESP:T05C12.10
A;Experimental source: clone M110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 31/3; 87/2; 141/3; 180/2; 203/3; 267/1; 776/2; 794/2; 834/2; 1086/3; 1143/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP:T05C12.10
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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 60; Conserv
  1119
                                                                                             1060 YAEKARKGECVLSIDESGEVIAD-EIVRVGRMINVGIYSPMTVEGSLIVDGVLSSCFSHL 1118
                                                                                                                                                                                     1001 EMFYHREPKTRINFYVLYTK-SGRKLSLIGRHLLPVAECSQVEQYIMNPDGIDVAMRESK 1059
                                             348 ESHQWAHR 355
                                                                                                                      290 FARRLRAGDSVLA--PGGDALRÞARVARVAREEAVGVFAÞLTAHGTLLVNDVLASCYAVL 347
                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                   942 AVLADIPGAAGAAGGGRSNCFSADSLYTTYTGQKR-MDELQIGDYYLYPSSGNYLKYEKY 1000
                                                                                                                                                                                                                                                                                                                         185 SVKADNSLAVRAGG-----CFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 DSVLAPGGDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQ----- 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           860 D-NGKTLQLTAGHFIYATECRYLPSKNSSLLNSTPERYRHLIDTLPDDSETKLASQLKIG 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 9.3%; Score 193.5; DB 2;
Local Similarity 27.1%; Pred. No. 1.6e-07;
hes 59; Conservative 41; Mismatches 83;
                                                                                                                                                                                                                      LLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAARGPA-----PAPGDFA---PV 289
ESHS-AHK 1125
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                   8.9%; Score 186.5; DB 2;
31.9%; Pred. No. 7e-07;
ative 36; Mismatches 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z81142; PIDN:CAB03509.1; GSPDB:GN00023; CESP:ZK1037.10 A;Experimental source: clone ZK1037
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                                                                                                                                                                                 between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
    Developmental
  protein;
  Autocatalytic cleavage; Hydrolase; Protease;
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## ALIGNMENTS

SULT 1	
H_HUMAN	STANDARD: DRT: 396 AA
043323; Q15794;	
15-JUL-19	1. 38, Crea
15-JUL-1999	(Rel. 38,
	99 (Rel. 38, Last annotation update)
DHH.	HEUGEHOG FROIEIN FRECORSOR (UHH) (HHG-3).
	sapiens (Human).
Eukaryota	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthería;	Primates; Catarrhini; Hominidae; Homo.
SEOUENCE	FROM N.A.
Tate G.,	Endo Y., Mitsuya T.;
Submitted	Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
SEQUENCE	[2] SEQUENCE OF 85-178 FROM N.A.
TISSUE-KIDNEY;	DNEY;
Drummond	I.A.;
"Human de	"Human desert hedgehog.";
-i - FUNCT	FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
PATTE	PATTERNING EVENTS DURING DEVELOPMENT. MAY FUNCTION AS A
DEVEL	
-i- SUBCE	SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
CELL,	CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
CELL	CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM
-i- PIM:	PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
AND A	A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN
3 🖺	CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF
	CHOOLESTEROF MOTERIA TO THE CITEMATURE OF THE NEWEL GENERALED N
TO PL	TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION
	PROTEIN ACTIVITY TO THE CELL SURFACE.
ACTIVE	'E SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
C-PRO	C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
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This SWIS	SWISS-PROT entry is copyright. It is produced through a collaboration

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Best Local Sim
Matches 396;
                                     MEDLINE: 94094334.

Echelard Y., Epstein D.J., St Jac Echelard Y., Epstein D.J., St Jac McMahon J.A., McMahon A.P.;

"Sonic hedgehog, a member of a famolecules, is implicated in the regular Cell 75:1417-1430(1993).
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15-JUL-1999 (Rel. 38, Last sequence update)
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                                                                                                                                                                                                                                          Metazoa;
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ilarity 100.0%;
Conservative
120-168 FROM N.A
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Sciurognathi; Murida
                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43577
                                                                                                                                                                                                                                                                                                    PRECURSOR (DHH) (HHG-3).
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DESERT HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
DESERT HED
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E -> G (IN REF. 2).
; FCE4FB21972C3AD5 CRC64;
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ESSENTIAL FOR AUTO-CLEAVAGE
SIMILARITY).
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Pred. No. 1
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                                                             regulation
                                                                                                                                                                                                                          Muridae; Murinae;
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on of CNS
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                                                                                                                       Mohler J.,
                                                                                                                                                                                                                          Mus.
                                                                                                                                                                                                                                            Mammalia;
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Chang D.T., Lopez A., von Kessler D.P., Chiang Chang D.T., Lopez A., von Kessler D.P., Beachy P.A.; Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.; "Products, genetic linkage and limb patterning"
                                                                                                                                                                                                                                                                      BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF01079; Hint; 1.
PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
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-!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
-PATTERRING EVENTS DURLING DEVELOPMENT. MAY FUNCTION AS A
SPERMATOCYTE SURVIVAL FACTOR IN THE TESTES. ESSENTIAL FOR TESTES
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                  ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENT.
SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED
TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN ADULT TESTES. NOT EXPRESSED I
LIMB BUDS.
                                                                                                                  GPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPG
VRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRN
                            VRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRN 180
                                                           GPAEGRVTRGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPG
                                                                                                                                                                                              Similarity
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96.5%;
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DESERT HEDGEHOG PROTEIN C-PRODUCT
CLEAVAGE (AUTO-)
INVOLVED IN CHOLESTEROL TRANSFER
SIMILARITY).
                                                                                                                                                                                           Score 2008; DB 1;
Pred. No. 1.1e-162;
                                                                                                                                                                                                                                                      CHOLESTEROL (BY SIMILARIT AFFEB051BE950FD8 CRC64;
                                                                                                                                                                                                                                                                                   SIMILARITY).
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ESSENTIAL F
                                                                                                                                                                                                                                                                                                                                INVOLVED IN AUTO-CLEAVAGE (BY
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                                                                                                                                                                                                                                                                      (BY SIMILARITY)
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PRODUCT
PROTEIN C-PRODUCT
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                                                                                                                                                                                                           Length 396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              gene family of xenopus laevis.";
Development 121:2337-2347(1995).
-i- FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTER ANTERODORSAL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES CEMENT GLAND FORMATION IN EMBRYOS.
-i- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM CELL, WHILE THE MTERMINAL PEPTIDE REMAINS ASSOCIATED WITH CELL SURFACE. HEDGENGG PROTEIN IS ALSO SECRETED IN EITHER COR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DESERT HEDGEHOG PROTEIN PRECURSOR 1 (DHH-1) (CEPHALIC
                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moon R.T., Beachy P.A.;
"Distinct expression and shared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHH1_XENLA
Q91610;
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                                      EMBL;
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                                                                                                                                                                                                    NEURULA EXPRESSION BECOMES RESTRICTED TO ANTERIOR STRUCTURES, ENCOMPASSING BOTH NEURAL PLATE AND ENDODERMAL CELLS.

PYM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODLFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE: DETECTABLE WITHIN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
     ; U26349; AAA85163.1; -.; PF01079; Hint; 1.; PF01085; HH_signal; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95401852.
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; Hint; 1.
; HH_signal;
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ea; Pipidae;
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                                                                                      http://www.isb-sib.ch/announce/
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Xenopodinae;
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S. INDUCES ECTO
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                                                                                                                                      restrictions
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Best Local Simi
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Developmental protein; Autoc
Signal.
SIGNAL 1 22
CHAIN 23 396
CHAIN 23 197
CHAIN 198 396
CHAIN 198 396
SITE 197 198
SITE 197 198
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DHH2_XENLA
Q91611;
15-JUL-1999
15-JUL-1999
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SEQUENCE
                                                                                                                                                                                                                 Eukaryota;
Batrachia;
MEDLINE; 95401852.
Ekker S.C., McGrew L.L., Lai C.-,
Moon R.T., Beachy P.A.;
"Distinct expression and shared a
gene family of Xenopus laevis.";
Development 121:2337-2347(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                 TISSUE-EMBRYO
                                                                                                                                                                                                                                                            Xenopus
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                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                             xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLLHA
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                                                                                                                                                                                                                                                                                                                        -1999 (Rel. 38, Created)
-1999 (Rel. 38, Last sequence update)
-1999 (Rel. 38, Last annotation updat
HEDGEHOG PROTEIN PRECURSOR 2 (DHH-2)
                                                                                                                                                                                                           laevis (African clawed frog).
ta; Metazoa; Chordata; Craniata; Vertebrata;
ia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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63.6%;
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                                                                                  Lai C.-J.,
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DESERT HEDGEHOG PROTEIN 1 C-PI
DESERT HEDGEHOG PROTEIN 1 C-PI
CLEAVAGE (AUTO-) (BY SIMILARI'
INVOLVED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-SER.
774A3EC2268A5EE9
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ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
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                                            activities
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                                                                                       Lee
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                                                                                                                                                                                                                                                                                                                        (DHH-2) (HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                   398
                                                                                                                                                                                                                                                                                                                                                update)
                                                                                  J.J.,
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PROTEIN 1 N-PRODUCT.
PROTEIN 1 C-PRODUCT.
) (BY SIMILARITY).
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                                              members
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                                                                                       Kessler
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                                                                                                                                                                                                               Amphibia;
Xenopodinae;
                                            of
                                                                                                                                                                                                                                                                                                                          PROTEIN
                                            the hedgehog
                                                                                         D.P.,
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Matches 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF01079; Hint; 1.
PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTERNING OF ANTERODORSAL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS.

SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. HEDGEHOG PROTEIN IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
TEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYESRNHVHVS 185
                                                                                                                                                                                                                                                                                                                                                               RVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMMPGVRLRV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLPLCCLALLALPAQSCGPGRGPV-GRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEG 65
                                                                                                                                                                                VKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDR 245
                                                                                                                                                                                                                                                                                                                                          KIRRGSERFIKLVPNYNPDIIFKDEENTGADRLMTERCKDRVNALAISVMNMWPGLKLRV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                ILAACCCWLLLLPVRCCGPGRGPVGGRRRYMRR-LVPLLYKQFVPNVPEKTLGASGKSEG
                                                                     DPYKTATFVLIEAEGHPTKLLVTPNHLLFIKSSSSTG---
                                                                                                             DLQRRASEVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSV-LAPG
                                                                                                                                                           VNTDNSLGVRSGGCFPGTAMVMMETGKKKPLSELKLGDTVFTTDETGLLIHSVVLLFLHR
                                                                                                                                                                                                                                                  TEGWDEDGHHAHDSLHYEGRALDITTSDRDRNKYGMLARLAVEAGFDWVYYESKAHIHVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1255.5;
Pred. No. 5.6e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESERT HEDGEHOG PROTEIN 2.
DESERT HEDGEHOG PROTEIN 2 N-PRODUCT.
DESERT HEDGEHOG PROTEIN 2 C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESSENTIAL FOR AUTO-CLEAVAGE SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHOLESTEROL (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DBC23AF85F69DD08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6e-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88;
                                                                     FQPTFAYRVQIGDLIQIYVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHH_MOUSE
Q62226;
                                                                                                                                                                                                                          MEDLINE; 96069744.

Hall T.M.T., Porter J.A., Beachy P.A.

"A potential catalytic site revealed
the amino-terminal signalling domain
Nature 378:212-216(1995).

-i- FUNCTION: BINDS TO THE PATCHED (P
                                                                                                                                                                                                                                                                                                                                                            the amino-terminal cleavage product of sonic hedgehog autoproteolysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecules, is implicated in the Cell 75:1417-1430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94094334.
Echelard Y., Epstein D.J.,
McMahon J.A., McMahon A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SONIC HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                        Roelink H., Porter J.A., Chiang C., Tanabe Y., Beachy P.A., Jessell T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE MEDLINE; 95254654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chang D.T., Lopez A., von Kessler D.P., Ch
Zhao R., Seldin M.F., Fallon J.F., Beachy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE MEDLINE; 95236997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McMahon A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McMahon J.A., McMahon A.F.;
"Sonic hedgehog, a member of a family of putative signaling"
"Sonic hedgehog, a member of a family of constitution of CNS polarity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHH OR HHG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999
15-JUL-1999
                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF
                                                                                                                                                                                                                                                                                                                                               Cell 81:445-455(1995).
                                                                                                                                                                                                                                                                                                                                                                                           "Floor plate and motor neuron induction by different concentrations
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Development 120:3339-3353(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Products, genetic linkage and limb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISION TO 122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364
                                                   FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL FOR PATTERNING OF THE BAYDERIOR. POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. BISPLAYS BOTH FLOOR, PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION ISSUED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G
          SIMILARITY).
SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTQVQSSKVVRVSVDEQTGVYAPMTEHGTLLVDGVLTSCYATVESHTLAHASLAPLRLFQ 363
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(Rel.
(Rel.
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el. 38, Last sequence upd
el. 38, Last annotation u
PROTEIN PRECURSOR (SHH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                    Beachy P.A., Leahy D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           St Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patterning activity of a murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                       by the 1.7-A crystal structure of Sonic hedgehog.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393
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                                                                                                                                                                                                                                                                                                                   34-195
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1. TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF EMBRYONIC TISSUES INCLUDING THE NOTOCHORD, VENTRAL NEURAL TUBE, FLOOR PLATE, LUNG BUD, ZONE OF POLARIZING ACTIVITY AND POSTERIOR DISTAL MESENCHYME OF LIMBS. IN THE ADULT, EXPRESSED IN LUNG AND NEURAL RETINA.

1. DEVELOPMENTAL STAGE: FIRST DETECTABLE DURING GASTRULATION.

1. INDUCTION: BY RETINOLD ACID.

1. PIM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEMLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE CAPRODUCT HAS NO SIGNALING ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X76290; CAA53922.1; -. PDB; 1VHH; 29-JAN-96.
242
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                                                                                                                                                                           122
                                                                                                                                                                                                                                                           62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:98297; SHH.
                                                                                                             VHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLL
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                                                                                                                                                                    PAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGV 121
                                                                                                                                                                                                                                                                                                                                                LLARCELVILASSLLVCPGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTLGASG
                                                                                                                                                                                                                                                                                                                                                                                                LLPLCCLALLA----LPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASG
FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGP---SALFASRVRPG
                                         FLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA - - - - RGPAPAPGDFAPVFARRLRAG
                                                                                    IHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLRPGDRVLAADDQGRLLYSDFLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01079; Hint; 1.
PF01085; HH_signal; I
s; PR00632; SONICHHOG
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437
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58.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1214;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
SONIC HEDGEHOG PROTEIN.
SONIC HEDGEHOG PROTEIN N-PRODUCT.
SONIC HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
TN CHOLESTEROL TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHOLESTEROL (BY SIMILARITY)
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 2e-95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                           82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 437;
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298
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Q63673;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence upd.
15-JUL-1999 (Rel. 38, Last annotation upd.
SONIC HEDGEROG PROTEIN PRECURSOR (SHH).
                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homolog of hedgehog expressed cell 76:761-775(1994).
-!- FUNCTION: BINDS TO THE PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roelink H., Augsburger A., Heemskerk J.,
Ruiz I Altaba A., Tanabe Y., Placzek M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHH OR VHH-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-EMBRYONIC FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94170375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Floor plate and motor neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 TWLL 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 AHRAFAPFRLAHALLAALAPARTDGGGGGSIPAAQSATEARGAEPTAGIHWYSQLLYHIG
                                                                                                                                                        TISSUE SPECIFICITY: EXPRESSED IN THE NODE, NOTOCHORD, FLOOR PLATE, AND POSSTERIOR LIMB BUD MESENCHYME.

PM: THE C.TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER CARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLGAZION FOR PATTERNING OF THE ANTERIOR POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS
                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED. TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS I ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION SIMILARITY).
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(Rel. 38, Last sequence update)
(Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                induction by vhh-1, by the notochord.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Edlund
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Best Local
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                                         SHH_CHICK STANDARD;
091035;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
SEQUENCE
    Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata;
Neognathae; Galliformes; Phasianidae; Ph
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Neognathae;
                                    SONIC
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                                                                                                              TWLL 422
                                                                                                                                                                       QRVYVVAERGGDRRLLPAAVHSVTLREEAAGAYAPLTADGTILINRVLASCYAVIEEHSW
                                                                                                                            EELL 395
                                                                                                                                                                                                                                                               AHRAFAPLRILHA-LGALLPG--------GAVQPTGMHWYSRLLYRLA
                                                                                                                                                                                DSVLA---PGGD-ALRPARVARVA-REEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQW 352
                                                                                                                                                                                                                                 PAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGV 121
                                                                                                                                          AHRAFAPFRLAHALLAALAPARTDGGGGGSIPAPQSVAEARGAGPPAGIHWYSQLLYHIG 418
                                                                                                                                                                                                     FLDRDEGAKKVFYVIETREPRERLLLTAAHLLEVAPHNDSGPTPGP---SPLFASRVRPG
                                                                                                                                                                                                                   FLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA----RGPAPAPGDFAPVFARRLRAG
                                                                                                                                                                                                                                                 VHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLL 241
                                                                                                                                                                                                                                                                                            RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV 121
                                                                                                                                                                                                                                                                                                                         LLARCFLVALASSLLVCPGLACGPGRG-FGKRQHPKK-LTPLAYKQFIPNVAEKTLGASG 61
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PF01079; Hint; 1.
PF01085; HH_signa
                                    HEDGEHOG
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383
437
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2; SONICHHOG.
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57.8%;
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                                   , Last sequence of Last annotation IN PRECURSOR (SHI
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                                                                                                                                                                                                                                                                                                                                                       Score 1203; D
Pred. No. 1.7e
52; Mismatches
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INVOLVED IN CHOLESTEROL TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLY.
0DBFC19F0D1662A0
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                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
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                                                                         425
       Phasianinae;
              Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                           CRC64
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       Gallus
              Archosauria;
                                                                                                                                                                                                                                                                                                                                                       40;
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                                                                                                                                                                                                                                                                                                                                                      Gaps
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PFAM;
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TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

IT ISSUE SPECIFICITY: EXPRESSED IN THE POSTERIOR LIMB BUD MESENCHYME, THE HENSEN'S NODE, THE NOTCHORD, AND THE FLOOR PLATE OF THE NUTLATIONS. THE HENSEN'S NODE, THE NOTCHORD, AND THE FLOOR PLATE OF THE NUTLATION OF LIMB BUD FORMATION. FROM THAT POINT ONWARDS, THE EXPRESSION PATTERN EXACTLY MATCHES THE LOCATION OF THE ZONE OF POLARIZING ACTIVITY (ZPA).

INDUCTION: BY RETINOID ACID.

INDUCTION: BY RETINOID ACID.

AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRACKENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS OF THE PROTEIN ACTIVITY OF THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY.

SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
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SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE WHITH THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE WHITH THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE WHITH THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHITH THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHITH THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL WHITH THE N-TERMINAL PEPTIDE DIFFUSES FR
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Riddle R.D., Johnson R.L., La
"Sonic hedgehog mediates the
Cell 75:1401-1416(1993).
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-!- FUNCTION: BINDS TO THE PATCHED (PTC)
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Beachy P.A., Jessell T.M.
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                                                                                                                                                                                                                                                                                                                                                                                                            Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Floor plate and motor neuron induction by different concentrations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE MEDLINE; 95254654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF01079; Hint; 1. PF01085; HH_signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR00632;
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27
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                                                                                                         SONIC HEDGEHOG PROTEIN.
SONIC HEDGEHOG PROTEIN C-PRODUCT
SONIC HEDGEHOG PROTEIN C-PRODUCT
CLEAVAGE (AUTO-) (PROBABLE).
INVOLVED IN CHOLESTEROL TRANSFER
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polarizing activity
SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE
SIMILARITY).
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RESULT 8
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Best Local Similarity
Matches 244; Conserv
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                       Marigo V., Roberts D.J., Lee S.M.K., Tsukurov O., Levi T., Gastier J.M., Epstein D.J., Gilbert D.J., Copeland N.G., Seidman C., Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C., "Cloning, expression, and chromosomal location of SHH and IHH: two human homologues of the Drosophila segment polarity gene hedgehog." Genomics 28:44-51(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SONIC HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q15465;
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     hedgehog
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 96070431
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-FETAL LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                              "Products, genetic linkage
                                                                                                   SEQUENCE OF 119-167 FROM MEDLINE; 95236997.
                                                                                                                                                                              Submitted (AUG-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QWAHRAFAPLRLLHA-LGALLPGGAV-----QPTGMHWYSRLLYRLAEELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKAHIHCSVKAENSVAAKSGGCFPGSATVHLEHGGTKLVKDLSPGDRVLAADADGRLLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVWNM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWAHWAFAPFRLAQGLLAALCPDGAIPTAATTTTGIHWYSRLLYRIGSWVL 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKPGQRVYVLGEGGQQLLPASVHSVSLREEASGAYAPLTAQGTILINRVLASCYAVIEEH
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                                                                            D.T.,
     gene.";
                                                   T., Lopez A.,
Seldin M.F.,
                                                                                                                                                                                                                            OF 1-187 FROM N.A.
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425
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(Rel.
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el. 38, Last sequence update)
el. 38, Last annotation update)
el. 78, Last annotation (HHG-1).
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393
46474
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                            von Kessler D.P., Chiang C.,
Fallon J.F., Beachy P.A.;
nkage and limb patterning act;
                                                                                                                                                                                                     Sutterer
                                                                                                                                                                              the
                                                                                                                             N.A.
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                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1198; DB 1;
Pred. No. 4.4e-94;
""matches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESSENTIAL FOR AUTO-CLEAVAGE SIMILARITY).
CHOLESTEROL (BY SIMILARITY).
POLY-THR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462
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                            activity of a murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 425;
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                                                                            Simandl B.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395
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     EMBL; AC002484;
MIM; 600725;
MIM; 142945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FINEL NOT EXPRESSED IN ADULT TISSUES.

-I- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHENT OF A CHOLESTEROL MOLETY TO THE C-TERMINAL OF THE NEWLY&GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

-I- DISCASE: DEFECTS IN SHH ARE THE CAUSE OF THE AUTOSOMAL DOMINANT DISCASE: DEFECTS IN SHH ARE THE CAUSE OF THE AUTOSOMAL DOMINANT DISCASE: DEFECTS THAT AFFECTS THE MIDLINE DEVELOPMENT OF THE FOREBRAIN AND MIDFACE. HPE IS ASSOCIATED WITH SEVERAL DISTINCT FACIES AND PHENOTYPIC VARIABILITY. IN THE MOST EXTREME CASES, ANOPHTHALMIA OR CYCLOPIA IS EVIDENT ALONG WITH A CONGENITAL ABSENCE OF THE MATURE NOSE. THE LESS SEVERE FORM FEATURES FACIAL DYSMORPHIA CHARACTERIZED BY OCCULAR HYPERTELORISM, DEFECTS OF THE UPPER LAILOR WITH A CONGENITAL DEPERT ALONG WITH A CONGENITAL DEPERT AND/OR NOSE, AND ABSENCE OF THE OLFACTORY NERVES OR CORPUS CALLOSIM
                                                Signal;
SIGNAL
CHAIN
CHAIN
CHAIN
SITE
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wrong the superior of the state of the superior of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          PFAM;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L38518;
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-!- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roessler E., Belloni E
Tsui L.-C., Muenke M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Development 120:3339-3353(1994).
                                                                                                                                                                                                                       Developmental
                                                                                                                                                                                                                                                                                                 PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSOCIATION WITH SMOOTHENED (SMÓ), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR. POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE-AND MOTOR NEURON-INDUCINED FOR MOTOR NEURON INDUCTION IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THI CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN FETAL INTESTINE, LIVER, LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORPUS CALLOSUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                           PF01079; Hint; 1.
PF01085; HH_signal; 1
S; PR00632; SONICHHOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPE3 ARG-31; GLY-117 AND ARG-117. 97051937.
                                                                                                                                                                                                                                                                                                                                                                      AAA62179.1; -
4; AAB67604.1;
                                                                                                                                                                                                                    protein; Autocatalytic cleavage; Hydrolase;
                                                                                                                                                                                                mutation.
                                              23
462
197
462
198
243
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                                                                                                                                                                                                                                                                     ۲.
                                           SONIC HEDGEHOG PROTEIN N-PRODUCT
SONIC HEDGEHOG PROTEIN C-PRODUCT
CLEAVAGE (AUTO-) (BY SIMILARITY)
INVOLVED IN CHOLESTEROL TRANSFER
                                                                                                                                            POTENTIAL.
SONIC HEDGEHOG PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PTC) RECEPTOR, WHICH FUNCTIONS II
AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berta
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                                                                                                                                                                                                                       Protease;
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MEDLINE; 900
                                                                                                                                                                                                                                                                                                                                    IHH_HUMAN STANDARD; PRT; 411 AA. 014623; 043322; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Fast annotation update) 15-JUL-1999 (Rel. 38, Fast annotation update) 10-JUL-1999 (Rel. 38, Fast annotatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
                                                                                                                         SEQUENCE FROM N.A.
Tate G., Endo Y., Mits.
"Human Indian Hedgehog
Submitted (SEP-1998) t
                                                                                                                                                                                                                                                Eukaryota;
Eutheria; I
                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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       Roberts D.J.,
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Catarrhini;
                                                                               FROM
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       Lee S.M.K.,
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W -> R /TV
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Pred. No. 3e-92;
4; Mismatches
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ESSENTIAL FOR AUTO-CLEAVAGE
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         Tsukurov
  0.
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       Levi
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EMBL;
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PATIENNING EVENIS DURING DEVENOUSED IN ENDOUGH PRACEDOR. WHICH FUNCTIONS IT ASSOCIATION WITH SMOOTHERED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN ENDOCHONDRAL OSSIFICATION. MAY REGULATE THE BALANCE BETWEEN GROWTH AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION OF PARATHYROID HORMONE-RELATED PROTEIN (PTHRP) (BY SIMILARITY).

1. SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL SURFACE. IS ALSO SECRETED IN ETHIER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

1. TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC LUNG, AND IN ADOLT KINNEY AND LIVER.

1. PIM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVED OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED NETERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (SIMILARITY).

1. SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gastler J.M., Epstein D.J., Gilbert D.J., Copeland N.G., Seidman C. Jenkins N.A., Seidman J.G., McWahon A.P., Tabin C.; "Cloning, expression, and chromosomal location of SHH and IHH: two human homologues of the Drosophila segment polarity gene hedgehog." Genomics 28:44-51(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandi B.K., Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.; "Products, genetic linkage and limb patterning activity of a murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development 120:3339-3353(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB018076;
AB018075;
AB010092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF01079; Hint; 1. PF01085; HH_signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L38517; AAA62178.1;
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; BAA33523.1;
; BAA33523.1;
202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Autocatalytic cleavage; Hydrolase;
                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOINED.
                CHOLESTEROL (BY SIMILARITY)
D -> R (IN REF. 2).
IIL -> LIF (IN REF. 2).
F -> V (IN REF. 2).
; 7888AC6B8C0B5647 CRC64;
                                                                                                                                                                                                                                                                                     INDIAN HEDGEHOG PROTEIN.
INDIAN HEDGEHOG PROTEIN N-PRODUCT.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER ()
                                                                                                                                                   ESSENTIAL FOR AUTO-CLEAVAGE SIMILARITY)
                                                                                                                                                                                                           SIMILARITY)
                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                          INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ght. It is produced through a collaboration - Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                       IN AUTO-CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no rest
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THE PATCHED
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Score 1161.5;

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Length 411;

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Best Local Similarity Matches 231; Conserv
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                                                                                                                                                                                                                                                                                                      and PTH-related protein.";

Science 273:613-622(1996).

Science 273:613-622(1996).

FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PURCTION: INTERCELULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PT RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO) ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GRAND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSI OF PARAMYROID HORMONE-RELATED PROTEIN (PTHRP).

-!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL, SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
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     TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING MIDGUT, LUNG AND CARTILAGE OF DEVELOPING LONG BONES IN THE LIMB.

PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTECLYSIS ACTIVITY AND A CHOLESTEROL TRANSPERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRDLQ 248
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ROTEIN PRECURSOR (IHH).
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8; Mismatches
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IHH_MOUSE STANDARD; PRT; 411 AA. P97812; Q61724; P9781299 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Fast annotation update) INDIAN HEDGEHOG PROTEIN PRECURSOR (IHH) (HHG-2).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGV 121
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INDIAN HEDGEHOG PROTEIN N-PRODUCT.
INDIAN HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
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Pred. No. 6.9e-91;
0; Mismatches 107
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CHOLESTEROL (BY SIMILARITY)
BA397AE2A9357A24 CRC64;
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PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC)
PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC)
RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN
ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH
AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION
OF PARATHYROID HORMONE-RELATED PROTEIN (PTRR).

-I- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE
CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE
CELL, SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM
TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-I- TISSUE SPECIFICITY: IN THE EMBRYO, DETECTED IN THE DEVELOPING GUT,
THE GROWTH ZONE OF CARTILAGE OF DEVELOPING LONG BONES, EPITHELIUM
AND UROGENITAL SINUS. IN THE ADULT KIDNEY, FOUND IN PROXIMAL
CONVOLUTED AND PROXIMAL STRAIGHT TUBLLE.

-I- DEVELOPMENTAL STAGE: DETECTED AT 10 DAYS POST COITUM (DPC) IN
DEVELOPMENTAL STAGE: DETECTED AT 10 DAYS POST COITUM (DPC) IN
DEVELOPING GUT, AT 14.5 DAYS DPC IN THE CARFILLAGE PRIMORDIUM AND
IN THE DEVELOPING UROGENITAL SINUS. EXPRESSION INCREASES WITH
ADDITIONAL AGE IN KIDNEY AND DUODENUM, BECOMING MAXIMAL IN
ADDITIONAL AGE IN KIDNEY AND DUODENUM, BECOMING MAXIMAL IN
the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.lsb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.; "Products, genetic linkage and limb patterning activity of a mur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CD-1; TISSUMEDLINE; 97236802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE: 94094334.
Echelard Y., Epstein D.J., St Jacques B., Shen L., Mohler J., McMahon J.A., McMahon A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Products, genetic linkage hedgehog gene.";
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                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS
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"Sonic hedgehog, a member of a family of putative molecules, is implicated in the regulation of CNS cell 75:1417-1430(1993).
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                                                                                                                                                               PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOZETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL STRUCE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANCE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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Q90419;
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EMBL; X76291; CAA53923.1; -.
MGD; MGI:96533; IHH.
PFAM; PF01079; Hint; 1
PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
                     Cyprinoidea;
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neopterygii; Teleostei; Euteleostei; Ostariophysi; (
                                                    Brachydanio rerio (2ebrafish)
                                                                           TIGGY-WINKLE
SEQUENCE FROM N.A.,
                                                                  HHWT
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                                                                                                                                                                                                                                       GWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNHVHVSVK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                         CLFLLLLLVPAARGCGPGR-VVGSRRRPPRKLVPLAYKQFSPNVPEKTLGASGRYEGKI 71
                                                                                                                                                                                                      -GALLPGGAVQPTGMHWYSRLLYRLAEELL
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                      Cyprinidae; Rasborinae;
                                                                           HEDGEHOG
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                                                                                                                              STANDARD;
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                                                                                   Last sequence update)
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                                                                           PROTEIN PRECURSOR
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 AUTOPROTEOLYTIC CLEAVAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
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Pred. No. 2.3e
Pred. Mismatches
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INDIAN HEDGEHOG
INDIAN HEDGEHOG
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INVOLVED IN CHOLESTEROL TRANSFER (BY
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                                                     (Zebra
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                      Danio
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PROTEIN N-PRODUCT
PROTEIN C-PRODUCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 411;
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                                Cypriniformes;
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TISSUE=EMBRYO;

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TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLING OF THE NEURAL TUBE AND BRAIN. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAY INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DENCEPHALON. NOT DETECTED IN THE NOTOCHORD OR DEVELOPING FIN BUD.

THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT OF A CHOLESTEROL MOLETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAMENT (N-PRODUCT). THIS COVALENT MODIFICATION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).
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SEQUENCE
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SITE
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"Patterning activities of vertebrate hedgehog proteins in developing eye and brain.";
Curr. Biol. 5:944-955(1995).
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SIGNAL
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                         WDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYESRNHYHYSYKA 188
WDEDGHHLEESLHYEGRAVDITTSDRDKSKYGMLSRLAVEAGFDWVYYESKAHIHCSVKA
                                                                                        RGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEG 128
                                                                                                                                                                                           LCFISLLLTPCGLACGPGRG-YGKRRHPKK-LTPLAYKQFIPNVAEKTLGASGKYEGKIT
                                                                                                                                                                                                                                         LCCLALLALP-AQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEGRVA
                                                                                                                                                                                                                                                                                         al Similarity
223; Conser
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s; PR00632; SONICHHOG.
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                                                                                                                                                                                                                                                                                              Conservative
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201
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270
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416
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46576 MW;
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                                                                                                                                                                                                                                                                                            65;
                                                                                                                                                                                                                                                                                         Score 1154; D
Pred. No. 2.3e
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
CHOLESTEROL (BY SIMILARITY).
; 61EC2218309CFE59 CRC64;
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ESSENTIAL FOR AUTO-CLEAVAGE
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INVOLVED IN AUTO-CLEAVAGE (BY
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TIGGY-WINKLE HEDGEHOG
TIGGY-WINKLE HEDGEHOG
                                                                                                                                                                                                                                                                                            DB 1;
2.3e-90;
nes 94;
                                                                                                                                                                                                                                                                                                                                       Length 416;
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                                                                                                                                                                                                                                                                                            12;
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C-PRODUCT
                                                                                                                                                                                                                                                                                         Gaps
190
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BAA09657.1;

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RESULT SHH_CV SH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHH_CYNPY
SHH_CYNPY
SHH_CYNPY
Q90385;
Q90385;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Dast annotation update)
15-JUL-1999 (Rel. 38, Dast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).

SINGLELLUAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FOR TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-!- INDUCTION: ACTIVATED BY ACTIVIN, BASIC FIBROBLAST GROWTH FACTOR (BEGF) AND FORK HEAD.

-!- PTM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEDLYSIS ACTIVITY AND A CHOLESTEROL TRANSFERASE ACTIVITY. BOTH ACTIVITIES RESULT IN THE CLEAVAGE OF THE FULL-LENGTH PROTEIN AND COVALENT ATTACHMENT CAND A CHOLESTEROL MOISTY TO THE C-TERMINAL OF THE NEWLY GENERATED NATIONAL DEPRENCE
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOCHEM. BIOPHYS. Res. COMMUN. 218:395-401(1996).

-!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVED IN LIME FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takabatake T., Takahashi T.C., Inoue K., Ogawa "Activation of two Cynops genes, fork head and animal cap explants.";
                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 96136334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
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                                                                                                                                                                                                                                                                                                                                TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION APPEARS TO PLAY AN ESSENTIAL ROLE IN RESTRICTING THE SPATIAL DISTRIBUTION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE C-PRODUCT HAS NO SIGNALING ACTIVITY (BY SIMILARITY).

SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTWLFPARESNVNFQEDGIHWYSNMLFHIGSWLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNSLAVRAGGCEPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDRDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GA-LLPGGA----VQPTGMHWYSRLLYRLAEELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLKSVTVKRIYTEEHEGSFAPVTAHGTIIVDQVLASCYAVIENHKWAHWAFAPVRLCHKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCYAVLESHQWAHRAFAPLRLLHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRROFIVIETSEPFTKLTLTAAHLVFV--GNSSAASGITATFASNVKPGDTVLVWEDTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRASFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSVLA--PGGD 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENSVAAKSGGCFPGSGTVTLGDGTRKPIKDLKVGDRVLAADEKGNVLISDFIMFIDHDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Amphibia; Salamandroidea; Salamandridae; Cynops.
                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M., Takeshima K.;
                                                                                                                                                                                                 restrictions on
                                                                                                                                                                                                                   gh a collaboration
                                                                                                                                                                                                                                        collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248
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Best Local :
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                                                                                                                                                                                                        BRARE
                                                                                                                    SHH, BRARE STANDARD; PRT; 418 AA. 092008; 013170; 013171; 15-UUL-1999 (Rel. 38, Created) 15-UUL-1999 (Rel. 38, Last sequence update) 15-UUL-1999 (Rel. 38, Last annotation update)
   MEDLINE;
Roelink H
                                                                     Brachydanio rerio (Zebrafish) (Zebra danio).
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
SEQUENCE
                                                                                                                SONIC HEDGEHOG
SHH OR VHH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
CHAIN
CHAIN
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SITE
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PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
                          TISSUE-EMBRYO
                                                                Neopterygii;
Cyprinoidea;
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                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                        AVIEEHSWAHWAFAPLRV--GLGILSFFSPQDYSSHSPPAPSQSEGVHWYSEILYRIGTW
                                                                                                                                                                                                                                                                                                                              AVLESHQWAHRAFAPLRLLHALGAL-------LPGGAVQPTGMHWYSRLLYRLAEE
                                                                                                                                                                                                                                                                                                                                                        RSMFASSVRAGHRVLTVDREGRGLREATVERVYLEEATGAYAPVTAHGTVVIDRVLASCY
                                                                                                                                                                                                                                                                                                                                                                        ---FARRLRAGDSVLAPG--GDALRPARVARVAREEAVGVFAPLTAHGTLLVNDVLASCY
                                                                                                                                                                                                                                                                                                                                                                                                         DFLLFMDKEETVRKVFYVIETS--RERVRLTAAHLLFVGQAHPGNDSGGDFRSVFGSAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                  PVLLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFA--ARGPAPAPGDFAPV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMMM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILLRRVLLAGFIC -- ALLVPSGLSCGPGRGIGTRKRF -- KKLTPLAYKQFTPNVPEKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALLTNLLP----LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRNHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPGVKLRVTEGWDEDGHHFEESLHYEGRAVDITTSDRDRSKYGMLARLAAEAGFDWVYFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKAHIHCSVKAENSVAAKSGGCFPGSATVALEQGVRIPVKDLRPGDRVLAADGLGKLVYS
H., Augsburge
                                                                                                                                                                                                                                                                                395
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34; Conservative
               94170375.
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432
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27
201
200
268
                                                              Cyprinidae;
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 Α.,
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                                                                 Rasborinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Œ.
 Heemskerk J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
SONIC HEDGEHOG PROTEIN.
SONIC HEDGEHOG PROTEIN N-PRODUCT.
SONIC HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1131.5; DB
Pred. No. 1.9e-88;
7; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHOLESTEROL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESSENTIAL FOI
SIMILARITY).
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                                                                 Danio
                                                                                                                                       update)
                                                                                                                            (VHH-1).
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  Korzh
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 Norlin
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                                                                                                                                                                                                                                                                                                                                                                                344
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EMBL;

L27585; U30711; Z35669;

AAA20998.1; AAC59742.1; CAA84738.1;

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(See http://www.isb-sib

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or send an email to license@isb-sib.ch).

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SIMILARITY)

-!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

-!- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL TUBE AND BRAIN. ALSO FOUND IN THE NOTOCHORD AND IN DEVELOPING FIN BUD. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAT INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DIENCEPHALON.

-!- DEVELOPMENTAL STAGE: FIRST DETECTABLE IN THE INNER CELL LAYER OF THE EMBRYONIC SHIELD DURING GASTRULATION. BY 9.5 HRS OF DEVELOPMENT, EXPRESSED IN A CONTINUOUS BAND THAT EXTENDS FROM THE EMBRYONIC SHIELD DOMAIN BY 19.5 HRS OF PRESCOMPTIVE THE ANTESIOR BOUNDARY OF EXPRESSION BEING POSITIONED IN THE CENTER OF THE ANIMAL POLE ANTERIOR TO THE PRESCOUT IN THE CLEAVAGE OF THE PUBLICANIAN AUTOPROTEOLYSIS ACTIVITY AND A CHOLESTEROL MOIETY TO THE C-TERMINAL OF THE NEWLY GENERATED N-TERMINAL FRAGMENT (N-PRODUCT). THIS COVALENT MODIFICATION OF THE PROTEIN ACTIVITY TO THE CELL SURFACE. THE N-PRODUCT IS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE ACTIVE SPECIES IN BOTH LOCAL AND LONG-RANGE SIGNALING, WHEREAS THE SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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Dodd J.;
"Floor plate a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fietz M.J., Concordet J.-P., Barbosa R., Johnson McMahon A.P., Tabin C., Ingham P.W.;
"The hedgehog gene family in Drosophila and verte Development Suppl. 43-51(1994).
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Cell 76:761-775(1994).
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Curr. Biol. 5:944-955(1995).
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by the notochord.";
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          SEQUENCE FROM N.A. TISSUE-INTESTINE; MEDLINE; 95357169.
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Eukaryota; Metazoa; Chordata; C
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38, Last sequence update;
39, Last annotation update;
39, Last annotation (VHH-1);
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SONIC HEDGEHOG PI
SONIC HEDGEHOG PI
CLEAVAGE (AUTO-)
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Pred. No. 1.7e-87;
6; Mismatches 107
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                                                                                                                                     Amphibia;
Xenopodinae;
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EMBL; U26314; AAA85162.1; -.
EMBL; L35248; AAA49981.1; -.
PFAM; PF01079; Hint; 1.
PFAM; PF01085; HH_signal; 1.
PRINTS; PR00632; SONICHHOG.
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SIMILARITY SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).

1 TISSUE SPECIFICITY: STONGLY EXPRESSED IN NOTOCHORD AND NEURAL FLOOR PLATE DURING EMBRYOGENESIS. IN TADPOLE, HIGH EXPRESSION IS OBSERVED IN PANCREAS/STOMACH, MODERATE EXPRESSION IN TAIL, AND LOW EXPRESSION IN INTESTINE, BRAIN, AND HIND LIMB.

1 DEVELOPMENTAL STAGE: FIRST DETECTED AT THE NEURULA (STAGES 16-17).

FIRST PEAK OF EXPRESSION AROUND TADPOLE HATCHING (STAGES 33-40).

HIGH EXPRESSION OBSERVED IN INTESTINE AT THE CLIMAX OF MORPHOGENESIS (STAGES 60-62) WHEN INTESTINE EPITHELIAL UNDERGOES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Restrictions to floor plate induction by hedgehog and winged-helix genes in the neural tube of frog embryos.";

Mol. Cell. Neurosci. 6:106-121(1995).

-I- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVEL IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND INTERCED TO THE CENTRAL NER
        Signal.
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"Distinct expression and shared activities gene family of Xenopus laevis.";
Development 121:2337-2347(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMERYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
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INDUCTION: BY THYROID HORMONE.
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POTENTIAL.
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SONIC HEDGEHOG PROTEIN C-PRODUCT.
SONIC HEDGEHOG PROTEIN C-PRODUCT.
CLEAVAGE (AUTO-) (BY SIMILARITY).
INVOLVED IN AUTO-CLEAVAGE (BY
SIMILARITY).
SSENTIAL FOR AUTO-CLEAVAGE (BY
SIMILARITY).
3 X 8 AA TANDEM REPEATS OF Q-V-D-L-Q-S-H-
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N -> S (IN REF. 3).
; 73B4E4932FA2EFF2 CRC64;
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TQSLL -> NSNLCW (IN REF. 3).
DRXTWTLKAVKVEKVDLE -> ESQDHDLEGRGKWRRLILR
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021835 caenorhabdi
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## ALIGNMENTS

O57567 PRELIMINARY; PRT; 406 AA.
O57567;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HEDGEHOG SECKENT POLARITY HOMOLOG.
NOtophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Caudata; Salamandroidea; Salamandridae; Notophthalmus.

HSSP; Q62226; 1VHH.

PFAM; PF01085; HH\_signal; 1.

PFAM; PF01079; Hint; 1.

PRINTS; PR00632; SONICHHOG.

SEQUENCE 406 AA; 45072 MW;

9D0FFA76 CRC32;

SEQUENCE FROM N.A. SEQUENCE FROM N.A. STARK D.R., GATES P.B., BROCKES Dev. Dyn. 0:0-0(1998).
EMBL; AF047466; AAC03108.1; -.

J.P.,

FERRETTI P.;

245	186 VKSEHSAAAKTGGCFPARALATLESGEKIPIADLEPGHRVLCMDEGGRRTYSDFLTFLDR 245	VKSEHSAAAKTGGCFPARALATL	186	Дb
245	186 VKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLFLDR 245	VKADNSLAVRAGGCFPGNATVRL	186	Qy
185	126 TEGWDEDGHHSDESLHYEGRAVDITTSDRDRNKYGMLARLAAEAGFDWVYYESKAHIHCS 185	TEGWDEDGHHSDESLHYEGRAVD	126	Db
185	126 TEGWDEDGHHAODSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNHVHVS 185	TEGWDEDGHHAQDSLHYEGRALD	126	Qy
125	66 KIARNSERFKELTPNYNPDIIFKDEENTGADRIMTQRCKDRLNSLAISVMNQWPGVKLRV 125	KIARNSERFKELTPNYNPDIIFK	66	Db
125	66 RVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRV 125	RVARGSERFRDLVPNYNPDIIFK	66	Qy
65	LLAVACALLLGGPGALGCGPGRVIGRRPRPPRLIPLSYKQFLPHVPEKTLGASGRYEG 65	LLAVACALLLGGPGALGCGPGR-	8	ρb
65	7 LIPICCIALLALP-AQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEG 65	LLPLCCLALLALP-AQSCGPGRG	7	Qy
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Best Local Similarity
Matches 218; Conser
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"Retinoic acid given at late embryonic stage depresses sonic hedgehog
and Hoxd-4 expression in the pharyngeal area and induces skeletal
malformation in flounder (Paralichthys olivaceus) embryos.";
Dev. Growth Differ. 41:143-152(1999).
EMBL; AB029748; BAA82360.1;
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SHH.
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;

Pleuronectiformes; Pleuronectoidei; Bothidae; Paralichthys.
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Last sequence update)
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Best Local Similarity 53.8%;
Matches 225; Conservative
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                                                                                                                                                                                                                                                                   073803; PRELIMINARY;
073803; PRELIMINARY;
01-AUG-1998 (TIEMBLIEL 07,
01-AUG-1998 (TIEMBLIEL 07,
01-NOV-1999 (TIEMBLIEL 12,
                                                                                                                    Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Verteborata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Caudata; Salamandroidea; Salamandridae; I
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he EMBL/GenBank/DDBJ
1; -.
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SEQUENCE FROM N.A.
GELLNER K., BRENNER S.;
Submitted (MAR-1998) to the
EMBL; AF056116; AAC34384.1;

EMBL/GenBank/DDBJ

databases

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RESULT
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Best Local S
Matches 210
                                                                        Query Match
Best Local S
Matches 192
                                                                                                                                                                  SHIMELD S.M.;

SHIMELD S.M.;

Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; Y13858; CAA74169.1; -.

HSSP; 062226; 1VHH.

PFAM; PF01085; HH_signal; 1.

PFAM; PF01079; Hint; 1.

PRINTS; PR00632; SONICHHOG.

SEQUENCE 415 AA; 46765 MW; C5BAC408 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O17499 PRELIMINARY; PRT; 415 AA. 017499; 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last annotation update) AMPHIHH PROTEIN.
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PFAM; PF01085; HH_signal;
PFAM; PF01079; Hint; 1.
SEQUENCE 442 AA; 49286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Branchiostoma floridae (Florida lancelet) (Amphioxus)
Eukaryota; Metazoa; Chordata; Cephalochordata; Branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              амрнінн.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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nes 210; Conserv
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                                                                        Local Similarity
mes 192; Conser
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                                                                        44.0%;
llarity 48.7%;
Conservative 5
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                                                                             56;
                                                                        Score 919; DB
Pred. No. 7.4e-
56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 990; DB 13;
Pred. No. 2.4e-69;
i0; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D41AA57C CRC32;
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                                                                                          DB 5;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HERTZLER P.L., MCCLAY D.R.;
Submitted (APR-1998) to the EX
EMBL; AF059605, AAC15065.1;
HSSP; 062226; 1VHH.
HSSP; 062226; 1VHH.
FFAM; PF01079; H1.51; 1.
PFAM; PF01079; H1.51; 1.
PRINTS; PR00632; SONICHHOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           061676;
061676;
01-AUG-1998
01-AUG-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae; Lytechinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                               STLFYVIETE-DKTIVQLTPQHLIYVSERESNFDQSRA-VFASEVRTNQFVYTTAQNHDR
                                                                                                                         NSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLELDRDLQR: | : | | : : | : : | |
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                                                                                                                                                                                                                                                                                                                        GSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEGW 129
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                                                 RASFVAVETEWPPRKLLLTPWHLVFAARGPAPAPGDFAPVFARRLRAGDSVLAPGGD---
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                                                                                               SAAAKNSGGCFPGFSQAYLKNGRMISMLDIRVGDEVAVVNNNGELDYSDVIMIVHRKLND
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(TremBLrel. 07, Last sequence update)
(TremBLrel. 12, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 781.5; DB 5;
Pred. No. 3.5e-53;
55; Mismatches 141;
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Best Local S
Matches 123
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Q9WV29
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Q9WV29
Q1-NOV-1999 (Trembirel. 12, Created)
Q1-NOV-1999 (Trembirel. 12, Last sequence update)
Q1-NOV-1999 (Trembirel. 12, Last annotation update)
Q1-NOV-1999 (Trembirel. 12, Last annotation update)
INDIAN HEDGEHOG PROTEIN (FRAGMENT).
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Capordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY;
GARGES P.L., MEYER R.A. JR., BROWN C.A., PRICE D.K.;
"Indian hedgehog in rat.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF162914; AAD45372.1; -.
NON_TER 1
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"Desert hedgehog in the rat.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF148226; AAD31927.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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01-NOV-1999 (TIEMBLIEL.
DESERT HEDGEHOG PROTEIN
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Pred. No. 1.1e-44;
1; Mismatches 3
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24CF1044 CRC32
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DYGY,
D QYGY7;
AC QYGY7;
AC QYGY7;
DT 01-MAY-1999 (TIEMBLTel. 10, Last sequence upuacc,
DT 01-MAY-1999 (TIEMBLTel. 12, Last annotation update)
DT 01-NOV-1999 (TIEMBLTEL. 12, Last annotation update)
DE SONIC HEDGEHOG (FRAGMENT).
DE SONIC HEDGEHOG (FRAGMENT).
OS Ambystoma mexicanum (Axolot1).
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amp'
Fukaryota; Metazoa; Chordata; Ambystomatidae; Amb
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Best Local Similarity 65.5
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01-NOV-1999 (TIEMBLIEL 12,
01-NOV-1999 (TIEMBLIEL 12,
01-NOV-1999 (TIEMBLIEL 12,
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"Development of Stratum Intermedian and its Role as a Stationaling Structure During Odontogenesis.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF144100; AAD33926.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SONIC HEDGEHOG (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 LAVEAGFDWVYYESRNHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 YKQFVPGVPERTLGASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERVNALAIAVMNMWPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLAR 164
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107; Conserv
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77.5%;
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Last annotation update)
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Pred. No. 4.4e-41;
2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 624; DB 11;
Pred. No. 2.1e-41;
25; Mismatches 36
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Ambystoma
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Best Local S
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Best Local Similarity
Matches 108; Conser
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TOROK M.A., IZELIZUA-BELMONTE J.C., GA
TOROK M.A., IZELIZUA-BELMONTE J.C., GA
SUBMILTEG (OCT-1997) to the EMBL/GenE
EMBL; AF031480; AAD18128.1; -.
HSSP; Q62226; IVHH.
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Neobatrachia; Bufonoidea; Leptodactylidae;
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01-NOV-1999 (TIEMBLIE1. 12,
01-NOV-1999 (TIEMBLIE1. 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Differences in vertebrate limb development revealed direct developing frog E. coqui.", Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databas EMBL, AF113403; AAD23436.1; -.
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                                                                                                                                                                                                                                                                                                                                   VPGVPERTLGASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVN 108
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                                                                                                                                                                                                                                        ALATAVMNMWPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVE
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                                                                                                                       AGFDWYYYESKAHIHCSV
                                                                                                                                                                 AGFDWYYYESRNHVHVSV 186
                                                                                                                                                                                                                  ALAISVMNLWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRERSKYGMLARLAVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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138
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15751 MW;
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Pred. No. 1.3e
23; Mismatches
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EMBL/GenBank/DDBJ databases.
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Pred. No. 4.2e-40;
5; Mismatches 17
    PRT;
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.3e-39;
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124 RVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYESRNHVH

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  Query Match
Best Local s
Matches 77
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Best Local Sim
Matches 109;
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O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-NOY-1999 (TrEMBLrel. 12, Last annotation updat
HEDGEHOG PROTEIN (FRAGMENT).
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NON_TER
SEQUENCE
                                                               NON_TER
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01-JAN-1998 (TREMBLrel. 05, Created)
01-JAN-1998 (TREMBLrel. 05, Last seq
01-NOV-1999 (TREMBLREL. 12, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

KEYS D.N., LEWIS D.L., SELEGUE J.E.,

CATES J., SCOTT M.P.,

CATES J., SCOTT M.P.,
                                                                                                 Submitted (SEP-1997) to the EMBL; AB007129; BAA22368.1; HSSP; Q62226; IVHH.
                                                                                                                                                  SEQUENCE FROM STRAIN-BBRR;
                                                                                                                                                                                                                Oryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorpha;
                                                                                                                                                                                                                                                                                                                             042128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF117742; AAD08931.1; HSSP; Q62226; 1VHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYS D.N., LEWIS D.L., SELEGUE J.E., PEARSON B.J., GOODRICH L.V.,
JOHNSON R.L., GATES J., SCOTT M.P., CARROLL S.B.;
"Recruitment of a hedgehog regulatory circuit in butterfly eyespot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Junonia coenia (Peacock butterfly) (Precis coenia).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; D1
Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
                                                                                                                                                                                          Oryzias.
                                                                                                                                                                                                    Cyprinodontiformes; Adrianichthyoidei; Adrianichthyidae; Oryziinae;
                                                                                                                                                                                                                                                      ME-SHH.
                                                                                                                                                                                                                                                                   HHS,
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                                                                                                                                         ARAKI K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                  179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASGPPEGRITRDDEKFRDLVPNYNPDIDFKDDEGTGADRLMTQRCKEKLNTLAISVMNQW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMW 118
                                                                                                                                                                                                                                                                                                                                                                                          RSYIHCSVKTESSVGTGA-GCFPSGAVVHTENGP-XDIASLKKGNKVLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYES 178
                                                                                                                                                                                                                                                                 PARTIAL
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                  Similarity
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4 119
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     Conservative
                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                     TISSUE-WHOLE
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                                                                 AA;
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                20.6%;
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                                                                                                                                                     EMBRYO;
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     23;
  Score 431; DB 1
Pred. No. 1.2e-2
23; Mismatches
                                                                                                                           EMBL/GenBank/DDBJ databases
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Pred. No. 2.4e-38;
6; Mismatches 33;
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                                                                 1CAE5021
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                                                                 CRC32;
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3 13;
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184 VSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLLF 242

RVTEGWDEDGHHFEESLHYEGRAVDITTSDRDKSKYGTLSRLAVEAGFDWVYYESKAHIH

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CSVKAESSVAAKSGGCFPGSSTVTLENGTQRPVKDLQPGDRVLAADYDGNPVYTDFINF 119

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                                                                                                              SEQUENCE FROM N.A. KOESTER R., STICK R., LOOSL SUBmitted (JUN-1997) to the EMBL; 297019; CAB09695.1; HSSP; Q62226; 1VHH. PRAM; PF01085; HH_Signal; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999
01-MAY-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (FRAGMENT).
SONIC HEDGEHOG (FRAGMENT).
Oryzias latipes (Medaka fish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Atherinomorpha;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorpha;
Neopterygii; Teleostei; Euteleostei; Adrianichthyidae; Oryziinae;
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MEDLINE; 99051425.
AMORES A., FORCE A., YAN Y.-I
HO R., AMEMIYA C., LANGELAND
POSTLETHWAIT J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Buteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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01-WAY-1999 (TIEMBLIEL 10, Last sequence update)
01-WOY-1999 (TIEMBLIEL 12, Last annotation updat
DESERT HEDGEHOG PROTEIN (FRAGMENT).
                                             NON_TER
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EMBL: AF071236; AAD15931.1; -
HSSP: Q62226; IVHH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 LLARLAVEAGFDWVYYESRNHVHVSVKA 188
|||:||||||||||:||: ||| |||
61 LLAQLAVEAGFDWVHYESKYHVHCSVKA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ERCKERVNALAIAVMNMWPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYG 160
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les 69; Conserv
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                                                                                                                                                                                                                                                                                      LOOSLI
                                                                                                                                                                                                                                         the
    MW;
                                                                                                                                                                                                                                         [ F., WITTBRODT J.;
EMBL/GenBank/DDBJ
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Pred. No. 1.9e-22;
7; Mismatches 12;
        59BE42B8 CRC32;
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Cypriniformes;
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Matches
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       ITTSDRDRNKYGLLARLAVE 168
ITTSDRDKSKYGTLSRLAVE
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61; Conserv
                                                    Conservative
                                                          16.9%;
76.2%;
80
                                                    15;
                                                    Score 352; DB 1:
Pred. No. 1e-20;
5; Mismatches
                                                                 DB 13;
                                                                Length 80;
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Post-processing: Minimum Match 0% Listing first 45 summaries
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length: 1000000
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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2088
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US-08-356-060A-35
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                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-176-427B-4
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,4271
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006
TELEPHONE: (617) 227-7400
TELEPAN: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                        Query Match
Best Local Sim
Matches 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08176427B Patent No. 5789543 GENERAL INFORMATION:
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APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: MA
COUNTRY: US.
ZIP: 02109
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US-08-748-591-8

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Pred. No. 2.5e-214;
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Result No.

Score

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                                                                                   ; MOLECULE TYPE: protein
US-08-356-060A-9
                                                                                                                          APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELEFONMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acids
TYPE: amino acids
Query Match
Best Local Similarity
Matches 382; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08356060A Patent No. 5844079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: McMahon, Andrew P.
APPLICANT: McMahon, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/356,060A FILING DATE: 14-DEC-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
   Conservative
             96.2%;
Score 2008; DB 2;
Pred. No. 2.5e-214;
6; Mismatches 8;
                                                                                                                                                                                                                                                 HMI-006CP
                              Length 396;
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US-08-176-427B-8
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                                                                               SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P:
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: HMI-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ingham, Phillip W. APPLICANT: McMahon, Andrew P. APPLICANT: Tabin, Clifford J.
 MOLECULE TYPE:
                                                SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 33
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              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                              437 amino acids
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protein
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US-08-356-060A-11

; Sequence 11, Application US/08356060A

; Patent No. 5844079
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Best Local Similarity
                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Vertebrate Embryonic Pattern-Induc
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                            Boston
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PCT-US95-15463-20
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GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 249; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                       ADDKL.
STREET:
La Jou
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                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                              ZIP: 92037
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                                                       FILING DATE: 0:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV 121
                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & RICHALUSUM ... STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 PAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LLARCFLVILASSLLVCPGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTLGASG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LLPLCCLALLA-----LPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA----RGPAPAPGDFAPVFARRLRAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EELL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLDRDEGAKKVFYVIETLEPRERLLLTAAHLLFVAPHNDSGPTPGP---SALFASRVRPG
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                                                                          01-DEC-1995
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                                                                                              PCT/US95/15463
   38,347
                                                                                                                                 Version #1.30
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ACTERISTICS:
437 amino acids
538 amino acids
7000LOGY: linear
648 amino acids
7000LOGY: 1500 acid
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; Sequence 20, Application PC/TUS9515923
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine,
; TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
; NUMBER OF SEQUENCES: 20
; NUMBER OF SEQUENCES: 20
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
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Best Local Similarity
                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: PCT/US95/15923
FILING DATE: 04-DEC-1995
                                                                                                                                                                                                                                 ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite
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                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 92037
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                           PCT-US95-02315-2
                                                                                                                                                                                                                                                                                                                                                                              RESULT
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INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                         Sequence 2, Application PC/TUS9502315
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M.
APPLICANT: Dodd, Jane
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Best Local :
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                                                                                                                                                       APPLICANT: ROELINK, HENK
APPLICANT: Editud, Thomas
TITLE OF INVENTION: HEDGEHC
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
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REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                              CORRESPONDENCE ADDRESS:
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NAME: Haile, Lisa A.
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                        419 TWLL 422
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||::||||::||||:||||||||
62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV 121
                               COUNTRY:
                                                         STATE:
                                                                            CITY: New York
                                                                                             ADDRESSEE: Cooper & STREET: 1185 Avenue
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les 248; Conserv
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                    10036
                                                       New York
                                       USA
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                                                                                                                                                                                            DNA ENCODING A VERTEBRATE HOMOLOG OF HEDGEHOG, VHH-1, EXPRESSED BY THE NOTOCHORD,
                                                                                                                                                                             THEREOF
                                                                                               Dunham of the
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REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 45375-A-PCT

TELECONMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEPAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid
                                                                                                                                                              Sequence 2, Application US/08176427B Patent No. 5789543
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Best Local Similarity
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                 GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.

APPLICANT: McMahon, Andrew P.

APPLICANT: Tabin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            419 TWLL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 IHCSVKAENSVAAKSDGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 VHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPVLL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 RYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/02315 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                  AHRAFAPLRLLHA-LGALLPG---------GAVQPTGMHWYSRLLYRLA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLDRDEGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSGPTPGP---SPLFASRVRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAR 181
                                                                                                                                                                                                                                                                                                                                                                           AHRAFAPFRLAHALLAALAPARTDGGGGGSIPAPQSVAEARGAGPPAGIHWYSQLLYHIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87; Indels
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Sequence 8, Application US/08356060A
; Patent No. 5844079
; GENERAL IMFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: MCMAhon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-427B-2
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US-08-356-060A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 425 amino acid
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STREET: 60
CITY: Bost
STATE: MA
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REFERENCE/DOCKET NUMBER: HMI-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MALLINLLP----LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKPGQRVYVLGEGGQQLLPASVHSVSLREEASGAYAPLTAQGTILINRVLASCYAVIEEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SRNHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPT 237
                                                                                                                                                                                                                         SWAHWAFAPFRLAQGLLAALCPDGAIPTAATTTTGIHWYSRLLYRIGSWVL 410
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                                                                                                                        us/08356060z
    Embryonic Pattern-Inducing
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TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-060A-8
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RESULT 10
US-08-748-591-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-DEC-1993
ATTORNEY/AGENY INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DC
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE 6
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                 118 WPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYE 177
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ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MALLTNLLP---LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLLLTRILLVGFIC--ALLVSSGLTCGPGRG-IGKRRHPKK-LTPLAYKQFIPNVAEKTL 59
                                                                                                QWAHRAFAPIRILHA-LGALLPGGAV-----QPTGMHWYSRLLYRLAEELL 395
                                                                                                                                                                                                                                                                                                  DFLTFLDRMDSSRKLFYVIETROPRARLLLTAAHLLFVAPQHNQSEATGSTSGQALFASN 299
                                                                                                                                                                                                                                                              PVLLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA - - RGPAPAPGDFA - - PVFARR 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQ 119
                                                                             SWAHWAFAPFRLAQGLLAALCPDGAIPTAATTTTGIHWYSRLLYRIGSWVL 410
                                                                                                                                                                                      LRAGDS--VLAPGGDALRPARVARVA-REEAVGVFAPLTAHGTLLVNDVLASCYAVLESH 350
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(617) 227-5941
R SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAHIVE & COCKFIELD
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30-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.4%; Score 1198; DB 2; 59.4%; Pred. No. 2e-124; tive 56; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/356,060A
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Sequence 4,

Application US/08748591

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NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE,/DOCKET NUMBER: 0651
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 322-5070
TELECTAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 245; Conserv
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GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Epstein, Ervin
APPLICANT: Hu, Zhilan
APPLICANT: Bonifas, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog Gene
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish and Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                180 NHYHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWYLAADASGRVVPTPV 239
                                                                                                                                                                                                                                                                                                                                                                             119
371
                                       358 RVLASCYAVIEEHSWAHRAFAPFRLAHALLAALAPARTDRGGDSGGGDRGGGGGGRVALTA 417
                                                                                                                                                                                                          239
                                                                                                                                                                                                                                                                                           179
                                                                                                                                                                                                                                                                                                                                                                                                 120 GVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYESR 179
                                                                                                                                                               285 DFAP--VFARRLRAGDSVLA----PGGDALRPARVARVA-REEAVGVFAPLTAHGTLLVN 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2200 Sand Hill Road CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                       ALGPRALFASRVRPGORVYVVAERDGDRRLLPAAVHSVTLSEEAAGAYAPLTAQGTILIN
                                                                                                                                                                                                                                                 LLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA------RGPAPAPG
                                                                                                                                                                                                                                                                                                                                                                         GVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLLLARCLLLVLVSSLLVCSGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTLGA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALLINLLPLCCL-ALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGA
PGGAVQP----TGMHWYSRLLYRLAEELL 395
                                                                              DVLASCYAVLESHQWAHRAFAPLRLLHALGALL-----
                                                                                                                                                                                                        LTFLDRDDGAKKVFYVIETREPRERLLLTAAHLLFVAPHNDSATGEPEASSGSGP-PSGG
                                                                                                                                                                                                                                                                                           AHIHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGRYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWP 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.4%; Score 1177; DB 1; 54.4%; Pred. No. 4.8e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/748,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54;
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,591
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 06510/067001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
metropany. (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.4%; Score 1177; DB 1; Best Local Similarity 54.4%; Pred. No. 4.8e-122; Matches 245; Conservative 54; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08748591 Patent No. 5759811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bonifas, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acid
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MEDIUM TYPE: Floppy disk
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285 DFAP--VFARRLRAGDSVLA----PGGDALRPARVARVA-REEAVGVFAPLTAHGTLLVN 337
                                                                                         240 LLFLDRDLQRRASFVAVETEWPPRKLLLTPWHLVFAA-------RGPAPAPG
                                                                                                                                   179 AHIHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDF 238
                                                                                                                                                                180 NHVHVSVKADNSLAVRAGGCFPGNATVRLWSGERKGLRELHRGDWVLAADASGRVVPTPV 239
                                                                                                                                                                                                                      119 GVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESK 178
                                                                                                                                                                                                                                           120 GVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWYYYESR 179
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APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
RUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: 1977777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: lin-
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APPLICATION NUMBER: US 0
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
119 GVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWYYYESK
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                                           120 GVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDRNKYGLLARLAVEAGFDWVYYESR 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 56.4%; Score 1177; DB 2; Length 47. Local Similarity 54.4%; Pred. No. 5e-122; nes 245; Conservative 54; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Vincent, Matthew REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 14-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                             1 MALLTNLLPLCCL-ALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGA 59
                                                                                                                                                                                                                                                                                                  1 MLLLARCLLLVLVSSLLVCSGLACGPGRG-FGKRRHPKK-LTPLAYKQFIPNVAEKTLGA 58
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                                                                                                                                                                                        SGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWP 119
                                                                                                                                                     SGRYEGKISRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWP 118
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30-DEC-1993
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; TOPOLOGY: both ; MOLECULE TYPE: p. PCT-US95-15463-19
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                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPAX: 619/678-5099
INFORMATION FOR SEQ. ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application PC/TUS9515463 GENERAL INFORMATION:
                                                                                                                                                          Matches 243;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOSIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Johns Hopkins University School of Medicine TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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                    58 GASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMM 117
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 01-DECCLASSIFICATION:
60 GASGRYEGKITRNSERFKELIPNYNPDIIFKDEENTGADRLMTCRCKDKLNALAISVMNC 119
                                                                                                                                                                            Local Similarity
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                                                                                                 MALLINILP---LCCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTL 57
                                                                           MILLTRILLVGFIC--ALLVSSGLTCGPGRG-IGHRRHPKK-LTPLAYKQFIPNVAEKTL 59
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4225 Execumery Square, Suite 1400
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                                                                                                                                                                        59.0%;
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                                                                                                                                                      %; Score 1158; DB 4;%; Pred. No. 5.4e-120;54; Mismatches 93;
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                                                                                                                                                                                          Length 425;
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                                                                                                                                                Query Match
Best Local Similarity
Matches 243; Conserv
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TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acids
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APPLICATION NUMBER: PC
FILING DATE: 04-DEC-19
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MEDIUM TYPE: Floppy disk
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                                      58
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Haile, Lisa A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 92037
                    GASGPAEGRVARGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMMM 117
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GASGRYEGKITRNSERFKELIPNYNPDIIFKDEENTGADRLMTCRCKDKLNALAISVMNC 119
                                                                                             RLRAGDS--VLAPGGDALRPARVARVA-REEAVGVFAPLTAHGTLLVNDVLASCYAVLES 349
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                                                                         MLLLTRILLVGFIC -- ALLVSSGLTCGPGRG-IGHRRHPKK-LTPLAYKQFIPNVAEKTL
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                                                                                                                                                    55.5%; score 1158; DB 4;
59.0%; Pred. No. 5.4e-120;
tive 54; Mismatches 93;
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                                                                                                                                                                                          Length 425;
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PCT-US95-15463-17
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                                                                                                                                                                                                             Query Match
Best Local :
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INFORMATION FOR SEO ID NO: 17:
SEQUENCE CHARACTERISTICS:
SOUTH AIR JAMINO ACIDS
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NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 HSWAHAAFAPHRLAQGLLAALCPDGAIPTAATTTTGIHWYSRLLYRIGSWVL 410
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ZIP: 92037
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   129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 01-DEC CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                       71
                                                                           69
                                                                                                                                  10 LCCLALLALP-AQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPGRTLGASGPAEGRVA 68
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STREET: 4225 Executive Square, Suite 1400
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 WDEDGHHAQDSLHYEGWALDITTSDRDRNKYGLLARLAVEAGFDWVYYESRNHVHVSVKA 188
                                                       RGSERFRDLVPNYNPDIIFKDEENSGADRLMTERCKERVNALAIAVMNMWPGVRLRVTEG 128
                                                                                                                LCFISLLLTPCGLACGPGRG-YGKRRHPKK-LTPLAYKQFIPNVAEKTLGASGKYEGKIT 70
                                     RNSERFKELIPNYNPDIIFKDEENTNADRLMTKRCKDKLNSLAISVMNHWPGVKLRVTEG 130
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                                                                                                                                                                                       55.3%; Score 1154; DB 4; 56.6%; Pred. No. 1.4e-119; tive 65; Mismatches 94;
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                                                                                                                                                                                                                           Length 416;
                                                                                                                                                                                       Indels
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MTWLFPARESNVNFQEDGIHWYSNMLFHIGSWLL 402
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Search completed: June 5, 2000, 08:17:16 Job time: 1300 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

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Query

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ALIGNMENTS

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4 M.musculus (129/Su) Dhh g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity [20] 75 (7), 1417-1430 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-NOV-1993) A.P. McMahon, Harvard Divinity Ave., Cambridge, MA 02138, USA 2 (bases 1 to 1191) Echelard, Y., Epstein, D.J., St-Jacques, B., Shermandhon, J.A. and McMahon, A.P.
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Vertebrate embryonic pattern-inducing
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Ingham, P.W., McMahon
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 TACAACCCCGACATCATCTTCAAGGATGAGGAGAACAGTGGAGCCGACCGCCTGATGACC
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1 (bases 1 to 1190)
Ingham,P.W., McMahon,A.P. and Tabin,C.
Vertebrate embryonic pattern-inducing
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                                                                                                  AC011603 241275 bp DNA Homo sapiens clone RP11-386G11, WORKING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-007-1999) Human Genome Sequencing Center, De of Molecular and Human Genetics, Baylor College of Medicin Baylor Plaza, Houston, TX 77030, USA on Feb 19, 2000 this sequence version replaced 91:6728920
                                                                                                                                                                                                                                                                                                                                                                                                              Direct/Submission
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                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 89 contigs. The true order of the pieces is not known and their order in this sequence record in
                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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2. contig of 910 bp in length
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2. contig of 820 bp in length
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3. contig of 825 bp in length
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9. contig of 766 bp in length
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ig of 775 bp in length
ig of 775 bp in length
ig of 910 bp in length
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ig of 820 bp in length
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                                                                                                                                                    GGTTTTGGCGGCCGATGCGTCAGGCCGGGTGGTGCCCACGCCGGTGCTGCTCTTCCTGGA 731
                                                                                                                                                                                                                 AACTGTGCGCCTGTGGAGCGGCGAGCGGAAAGGGCTGCGGGAAACTGCACCGCGGAGACTG
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g of 1485 bp in length
of unknown length
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32162 33672 33692 34585 34605 35545 35545 36661 37454

gap of contig gap of contig

25141 25161 26666 26686 28362 28382 29306 29326

30969

23144 23961 23981

19694 20611 20631 20631 21486 21506 22338 22338 22358

18113 18133 18953 18973 18973

13697 14553 14573 15550 15570 16388

gap of contig gap of contig gap of contig

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-FEB-1998) to the DDBJ/EMBL/GenBank databases. Genshi Tate, Showa University Fujigaoka Hospital, Department of Surgical Pathology; Fujigaoka 1-30, Aoba-ku, Yokohama, Kanagawa 227-8501, Japan (E-mail:six10352@super.win.or.jp, Tel:81-45-974-6632,
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Homo sapiens hedgehog (
AB010994
AB010994.1 GI:2887455
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J. Biochem. Mol. Biol. Biophys. 4, 27-34 (2000)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            /gene="hedgehog"
/number=3
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/db_xref="G1:2887457"
/db_xref="G1:2887457"
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CKERVUALALAVMNMWPGVRLRVTEGWDEDGHHAQDSLHYEGRALDITTSDRDNKYG
LLARLAVEAGFDWYYYESRNHVHVSVKADNELAVRAGGFPGNATVRLMSGERKGLRE
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LHRGDMVLAADASGRVVPIPVLFLFLDRDLQRRASFVARVAREEAVGVFAPLTAHGTL
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/oin(AB010581.1:1. .303,AB010993.1:1.
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/oin(AB010581.1:1. .303,AB010993.1:1.
/gene="hedgehog"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 1958)
Vortkamp, A., Lee, K., Lanske, B., Segre, G.V., Kronenberg, H.M. and
                                                        Regulation of rate of cartilage and PTH-related protein Science 273 (5275), 613-622 (199
 Tabin, C.J.
Direct Submission
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                       Segre, G.V.,
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GCGGCCGATGCGTCAGGCCGGGTGGTGCTGCTCCTTCCTGGACCGGGAC
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                                             ACGCTGGAGAACGGTGCCCGGACGCCACTGTGGGCACTGCGGCCCGGGCCAGCGGGTGCTG
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43; Conservative
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LVVDDVVASCFALVREQQLAQMAFWPLRLYHSLLGGPGVQGDGVHWYSGLLYRLGRML
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LRPGQRVLAMDGAGRPTYSDFLAFLDKEPRALTAFHVLETRQPPRRLALTPTHLLFVA
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Submitted (15-JAN-1997) Internal Medicine/Division of Nephrology,
University of Michigan Medical School, 1560 MSRB II--Box 0676, Ann
Arbor, MI 48109-0676, USA
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184. .1533
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PGVKLRVTEGWDEDGHHSEESLHYEGGAVDIITSDRDRNKYGLLARLAVEAGFDWYY
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TYGPGQYVLIFLDREPNRLRAFQVIETQDPRRLAITRGTLVEDVVASCFAAVADH
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Ingham, P.W., McMahon
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Ingham,P.W., McMahon,A.P. and Tabin,C
Vertebrate embryonic pattern-inducing
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Similarity 64.5%;
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Pred. No. 2.3e-61;
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                                                            AGAGTCACCAGTGGGCGCACCGCCTTTGCCCCCTTGAGACTGCTGCACGCGCTAGGGG
                                                                                              TCACGGCGCACGGCACCATTCTCATCAACCGGGTGCTCGCCTCGTGCTACGCTGTCATCG
                                                                                                                     TCACCGCGCACGGGACGCTGGTGAACGATGTCCTGGCCTCTTGCTACGCGGTTCTGG 1042
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M.musculus (C57BL/6J)
X76290
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Submitted (03-NOV-1997) A.P. McMahon, Harvard
Divinity Ave., Cambridge, MA 02138, USA
On Nov 8, 1997 this sequence version replaced
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Echelard,Y., Epstein,D.J., St-Jacques,B., Shen,L., Mohler, McMahon,J.A. and McMahon,A.P.
Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity Cell 75 (7), 1417-1430 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (24-NOV-1993) A.P. McMahon, H.
Divinity Ave., Cambridge, MA 02138, USA
revised by [3]
2 (bases 1 to 1314)
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McMahon, A.P.
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1 (bases 1 to 1314)
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shh gene; sonic hedgehog protein
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MLARLAVEAGFDWYYYESKAHIHCSVKAENSVAAKSGGCFPGSATVHLEQGGTKLVXD
LRPGDRVTAAADDGGRLLYSDFITFLDRDEGAKKVFVIETLEFERELLLTAAHLLFVA
PHNDSGPTPGPSALFASRVRFGQRVYTVVAERGGDRRLLPAAVHSVTLREEAGGYAPL
TAHGTILINRVLASCYAVIEEHSWAHRAFAPFELAHALLAALAPARTDGGGGGSIPAA
QSATEARGAEPTAGIHWYSQLLYHIGTWLLDSETMHPLGMAVKSS"
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/strain-"C57BL/63"
/db_xref-"taxon:10090"
/dev_stage-"embryo, 8.5 dpc"
/clone_lib-"Hogan; lambda gt10"
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/db_xref="GI:2597988"
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                                                                      CCGCTACTACAAGCAATTTGTGCCCGGCGTGCCAGAGCGGACCCTGGGCGCCAGTGGG
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                                                                                                                   TGTTGTGGTCCTGGCCGGGGGCCGGTTGGCGGCCGGCGCCGTTACATGAGGAGACTGGTC 126
                                                                                                                                                                                                                                                         693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1197)
Ekker, S.C., McGrew, L.L.,
Moon, R.T. and Beachy, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-MAY-1995) Stephen C. Ekker, Genetics, Johns Hopkins University, 725 N. Baltimore, MD 21205, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moon, R.T. and Beachy, P.A.
Distinct expression and shared activities of hedgehog gene family of Xenopus laevis Development 121 (8), 2337-2347 (1995)
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U26350
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93; Conservative
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/protein_id="hedgehog protein 4"
/protein_id="AAA85164.1"
/db_xref="GI:1147830"
/translation="mpavrilliaacccwilllpvrccgpgrgpvggrrrymrrlvpl
_tykQfVpNvpEkTLGASGKSEGKIRRGSERFIKLVPNYNPDIIIFKDEENTGAARLMTE
RCKDRVNALAISVMNMMPGLKLRVTEEWDEDGHHANGSLHYEGRALDITTSDRDRNKY
GMLARLAGFDWYYESKAHIHVSVWTDNSLGVRASGGFFFTAMVMMETGKKFLFS
ELKLGDTVFTTDETGLLIHSVVLLFLBRDPYKTATFYLJEAEGHPTKLLYPNHLTEI
KSSSTGFQPTFAYRVQIGDLIQIYVNGTQVQSSKVVRVSVDDQTGVVAPMTEHGTLL
VDGVLTSCYATVESHTLAHASLAPLRLFQGIASMLPDLHTSDGVHWYCHILYYLAKYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="related to Xenopus laevis cephalic hedgehog, encoded by GenBank Accession Number U26349; secreted signaling molecule; Method: conceptual translation supplied by author"
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/db_xref="taxon:8355"
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Mesobatrachia; Pipoidea; Pipidae;
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Pred. No. 1.2e-60;
0; Mismatches 409;
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Xenopodinae;
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Rat (vhh-1) mRNA,
L27340
L27340.1 GI:45212
Rattus norvegicus strain Sprague-Dawley
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata;
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                                                TGATGAACATGTGGCCCGGAGTGCCCCTACGAGTGACTGAGGGCTGGGACGAGGACGAGGACGGCC
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1 (bases 1 to 1715)

Roelink, H., Augsburger, A., Heemskerk, J., Korzh, V., Norlin, S.

1 Altaba, A., Tanabe, Y., Placzek, M., Edlund, T., Jessell, T.M.
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//Bb_xref="G1:452123"
//Bb_xref="G1:45212
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
315. .377
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315. .1628
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Pred. No. 3.1e-59;
D; Mismatches 370
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                                                                                                                                                                         Ekker, S.C., McGrew, L.L., Lai, C.J., Lee, J.J. Moon, R.T. and Beachy, P.A.
Distinct expression and shared activities hedgehog gene family of xenopus laevis Development 121 (8), 2337-2347 (1995)
                                               Submitted (04-MAY-1995) Stephen C. Ekker, Molecular Biology and Genetics, Johns Hopkins University, 725 N. Wolfe St, 714 PCTB, Baltimore, MD 21205, USA
                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis cephalic U26349
                                                                                                    Direct Submission
                                                                                                             2 (bases 1 to 1191)
Ekker, S.C., McGrew, L.L.,
Moon, R.T. and Beachy, P.A.
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                 African clawed frog
Xenopus laevis
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/organism="Xenopus laevis'
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/protein_id="AAA85163.1"
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/db_xref="GI:1147828"
/db_xref="GI:1147828"
/db_xref="GI:1147828"
/translation="mpayrivilaliccgilipvynynpdiifkDeekigaDrimterc
kOfvpnvpektigaSgkSegkiifkGeekfielvpvynpdiifkDeekigaDrimterc
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kDRVNALAISYUNMWPCYKLKYTEGWOEDGHHAHDSCHYEGRALDITTSDRDRNKYGM
LARLAVEAGFDWYYESKALIKYTEGWOEDGHHAHDSCHERGHSKLLVTPNHILF1028
KIGDTYTTDETGQLITSVVLLFLHRNPYKTATFVLIEAEGHSKLLVTPNHILF1028
SSSAGFLPTFAYRVQIGDLVQIYVNGTQVQSSKVVRVSLEEQTGVYADMTEHGTILVD
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translation supplied by author"
/codon_start=1
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                                              TCTACTGCCCTTGTGCTGCCTTGGCACTTCTGGCGCTGCCAGAGCTGCGGGCCGGG
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Ingham, P.W., McMahon, A.P. and Tabin, C.
Vertebrate embryonic pattern-inducing
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L38518.1 GI:663156
homologue; sonic hedgehog protein
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                                     bp mRNA
c hedgehog
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complete cds.
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Local Similarity 61.9%;
hes 711; Conservative
GGTGAACGCTTTGGCCATTGCCGTGATGAACATGTGGCCCGGAGTGCGCCTACGAGTGAC
                                                                                                                          CAGGGGGTTCGGGAAGAGGAGGCAC-----CCCAAAAAGCTGACCCCTTTAGCCTACAA
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                                                                                        CTTCAAGGATGAGGAGAACAGTGGAGCCGACCGCCTGATGACCGAGCGTTGCAAGGAGAG
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1576)
Marigo, V., Roberts, D.J., Lee, S.M.K., Tsukurov, O., Levi, T., Gastier, J.M., Epstein, D.J., Gilbert, D.J., Martin, G.G., Copeland, N.G., Seidman, C.E., Jenkins, N.A., Seidman, J.G., McMahon, A.P. and Tabin, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning, expression and chromosomal location of SHH and IHH, two human homologues of the Drosophila segment polarity gene Hedgehog Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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ALHPLGMAVKSS"
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152. .1540
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/tissue_lib="Clontech"
/note="vector: lambda |
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/db_xref="taxon:9606"
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1. .1576
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0; Mismatches 369;
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                        1095 GCTAGGGGC 1103
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                                                               GGTTCTGGAGAGTCACCAGTGGGCGCACCGCGCTTTTTGCCCCCCTTGAGACTGCTGCACGC 1094
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GCTCCTGGC 1314
                                                 GGTCATCGAGGAGCACAGCTGGGCGCACCGGGCCTTCGCGCCCTTCCGCCTGGCGCACGC 1305
                                                                                                                                                              -----TGGCGCGGAGGAAGCCGTGGGCGTGTT 974
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Search completed: June 5, 2000, 07:33:10 Job time: 9655 sec

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1622
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-356-060A-7
US-08-176-427B-1
US-08-356-060A-1
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US-08-356-060A-1
US-08-356-060A-1
US-08-748-591-10
US-08-748-591-17
US-08-748-591-17
US-08-356-060A-1
US-08-356-060A-1
US-08-356-060A-1
US-08-356-060A-1
US-08-356-060A-2
US-08-366-392A-1
US-08-366-392A-1
US-08-471-033-1
US-08-471-033-1
US-08-471-044-18
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 Sequence 1, A)
Sequence 1, A)
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Sequence 79,
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US-08-356-060A-7
; Sequence 7, App
                      US-08-356-060A-7
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US-08-471-046A-26	US-08-471-046A-17	US-08-463-483A-26	US-08-463-483A-17	US-08-471-044-26	US-08-471-044-17	US-08-471-033-26	US-08-471-033-17	US-08-469-334-35	US-08-470-566B-35	US-08-471-046A-35	US-08-463-483A-35	US-08-471-044-35	US-08-471-033-35	1	US-08-470-566B-18	US-08-471-046A-18	US-08-463-483A-18
•	Sequence 17, Appl	`	17,	`	`	`	•	`	`	`	`	Sequence 35, Appl	`	•	•	`	•

## ALIGNMENTS

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AFFLICATION: 435

FILING DATE: 14-DEC-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION UNMBER: US 08/176,427

FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REGISTRATION NUMBER: HMI-006CP

REFERENCE/DOCKET NUMBER: HMI-006CP

TELECOMMUNICATION: TOORMATION:

TELEPHONE: (617) 227-7400

TELEPHONE: (617) 227-740

TELEPHONE: (617) 227-740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
                                                 MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
ZIP: 021
NAME/KEY:
LOCATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     TOPOLOGY: lin
                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII(text)
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CITY: Boston
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Best Local Similarity
Matches 936; Conserv
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                                                                                                                         GAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTTTACGGCT 890
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                                        GTGCATTGGTACCCCCAGCTGCTCTACCGCCTGGGGGCGTCTCCTGCTAGAAGAGGGCAGC
                                                                                  TTCTGGCCCCTGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGT
                                                                                             TICTGGCCCCTGAGACTCTITCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGT
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TTCCACCCACTGGGCATGTCCGGGGCAGGGAGCTGA 939
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100.0%;
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; Pred. No. 1.7e-198;
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RESULT 2
US-08-176-427B-5
; Sequence 5, Application
; Patent No. 5789543

US/08176427B

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; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1056
US-08-176-4278-5
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-193
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006
TELECOMMUNICATION INFORMATION:
TELECPHONE: (617) 227-740
INFORMATION FOR SEQ ID NO: 5:
SECURACE CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 928
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ADDRESSEE: LAHIVE & COCI
STREET: 60 State Street
CITY: Boston
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APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1056 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 52.0%;
Local Similarity 88.2%;
nes 928; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: linear
GCCGCAGCCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCCAGGTACGCCTGGAGAGTGGG
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                                                                       GACTGGGTGTATTACGAGTCAAAGGCCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCG
                                                                                                                                             TCAGACCGCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAAGCCCGGCTTT 575
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                                                      GACTGGGTGTATTACGAGTCCAAGGCCCCACGTGCATTGCTCTGTCAAGTCTGAGCATTCG
                                                                                                                            TCAGACCGTGACCGAAATAAGTATGGACTGCTGGCGCGCTTAGCAGTGGAGGCCGGCTTC
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RESULT 3
US-08-356-060A-3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                 APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                           1021 AACCACTGCCCTCCTGGAACTGCTGTGCGTGG 1052
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                                                                                                                        ADDRESSEE:
STREET: 60
CITY: Bosto
STATE: MA
COUNTRY: US
ZIP: 02109
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                              CTGCTCTTTACGGCTGACAATCACACGGAGCCGGCAGCCCCCCTTCCGGGCCACATTTGCC
                                                                                         GCTTTCCAGGTCATCGAGACTCAGGATCCTCCGCGTCGGCTGGCGCTCACGCCTGCCCAC
                                                                                                                        GCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCGCTCAC
                                                                                                                                                       GGGACCCCCACCTTCAGTGATGTGCTTATTTTCCTGGACCGCGAGCCAAACCGGCTGAGA
                                                                                                                                                                     GGGAGCCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGA
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ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
I ENGREE CHARACTERISTICS:
I ENGREE CHARACTERISTICS:
MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                       TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                         LENGTH: 1056 base pairs
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Query Match Best Local Similarity Matches 928; Conserv 276 GAGCGCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAG TCAGACCGCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCAGTGGAGGCCGGCTTT 575 ATCTCGGTGATGAACCAGTGGCCCGGGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAG 455 AACACAGGCGCCGACCGCCTCATGACCCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCT 395 GACGGCCACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGGGTGGACATCACCACA 515 ATCTCTGTCATGAACCAGTGGCCTGGTGAAACTGCGGGTGACCGAAGGCCGGGATGAA 180 AACACGGGTGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGTCTGAACTCACTGGCC TCAGACCGTGACCGAAATAAGTATGGACTGCTGGCGCGCTTAGCAGTGGAGGCCGGCTTC GATGGCCATCACTCAGAGGAGTCTTTACACTATGAGGGCCGCGCGGGTGGATATCACCACC 52.0%; ilarity 88.2%; Conservative 0, Score 843.2; DE Pred. No. 5.5e-1 Mismatches 123; B Indels Length 1056; 1; Gaps 120 60 335 300 240

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; NAME/KEY:
; LOCATION:
US-08-176-427B-1
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US-08-176-427B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/081764278
Patent No. 5789543
GENERAL INFORMATION:
APPLICANT: Infoham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 33
CORRESSONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-941
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/176,4271

FILING DATE: 30-DEC-1993

CLASSIFICATION: 435
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                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
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                                                                     MOLECULE TYPE:
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CITY: Boston
STATE: MA
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                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Sim.
Matches 763;
 1067
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TCGAGGAGCACAGTTGGGCCCATTGGGCCTCGCACCATTCCGCTTGGCTCAGGGGCTGC
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                                                          CACTCACCGCCCAGGGCACCATCCTCATCAACCGGGTGTTGGCCTTCCTGCTACGCCGTCA
                                                                                                                       TGCTGCCGGCGTCTGTCCACAGCGTCTCATTGCGGGAGGCGTCCGGAGCCTACGCCCC
                                                                                                                                                                                                                  TTGCCAGCCACGTGCAGCCTGGCCA-----GTACGTGCTGGTGGCTGGGGTGCCAGGCC
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                              TGGCTGACCACCTGGCTCAGTTGGCCTTCTGGCCCCTGAGACTCTTTCACAGCTTGG
                                                                                         CGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGGTGGCATCCTGCTTCGCGGCCG
                                                                                                                                                    TGCAGCCTGCCCGCGTGGCAGCTGTCTCTACAC---ACGTGGCCCTCGGGGGCCTACGCCC
                                                                                                                                                                                    TTACGGCTGACAATCACACGGAGCCGG------CAGCCCGCTTCCGGGCCACAT
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Pred. No. 3.9e-93;
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US-08-356-060A-1
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                                                                                                                   Query Match
Best Local :
                                                                                                   Best Local Similarity Matches 763; Conserv
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APPLICANT: McMahon, Andrew P.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATÁ:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
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APPLICATION NUMBER: 1
FILING DATE: 30-DEC-
                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
   223
                                     107
                                                   163 GGCGACCGCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGCCCCCAATGTGCCCG 222
                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 60 St
CITY: Boston
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                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                  Score 459; DB 3; 1
Pred. No. 3.9e-93;
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                                                                                                                                  Length 1277;
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                                                                       ATTGGTACCCCCAGCTGCTCTACCGCCCTGGGGCGTCTCCTGCTAGAAGAAGAGGCCAGCTTCC
                                                                                                                   TGGCCGCCCTCTGCCCAGATGGGGCCATCCCTACTGCCGCCACCACCACCACTGGCATCC
                                                                                                                                                    CATGGGGCAGCTGGACCCCGGGGGAG----
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                                                 ATTEGTACTCACGGCTCCTCTACCGCATCGGCAGCTGGGTGCTGGATGGTGACGCGCTGC
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US-08-356-060A-6
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REFERENCE/DOCKET NUMBER: HMI-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1425 base pairs
TYPE: nucleic acid
STRANDEDNESS: 24-1-1
                                                                                                                                                                                                                                                                                                    Query Match 28.1
Best Local Similarity 71.1
Matches 631; Conservative
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GENERAL INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
DEFENSIOR NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing TITLE OF INVENTION: Proteins and Uses Related Thereto NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS: ADDRESS: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
205
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CITY: Boston
STATE: MA
COUNTRY: USA
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                                                                                                                                                                                   150 GTGGGCAGCCGCCGGCGACCGCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGC 209
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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NO. 5844079
AACTCCGAGCGATTTAAGGAACTCACCCCCAATTACAACCCCGACATCATATTTAAGGAT
                   AGCTCCGAGCGCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGAC 329
                                                                                            TTCGGGAAGAGGAGGCACCCCAAA----AAGCTGACCCCTTTAGCCTACAAGCAGTTTATC 144
                                                                                                                                                                                                                           CTAGTCCTCGTCTCCTCGCTGCTGCTATGCTCGGGACTGCCGACCGGCAGGGGG 87
                                                                         CCCAATGTGGCCGAGAAGACCCTAGGCGCCAGCGGAAGGTATGAAGGGAAGATCTCCAGA 204
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                                                                                                                                                                                                                                                                                                    Score 453.8; DB 3;
Pred. No. 5.6e-92;
0; Mismatches 252;
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US-08-748-591-5
; Sequence 5, Application US/08748591
; Patent No. 5759811
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                                                                                                                                                                                                                                                                           APPLICANT: Epstein, Ervin
APPLICANT: Hu, Zhilan
APPLICANT: Bonifas, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog Ge
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish and Richardson
STREET: 2200 Sand Hill Road
                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
               APPLICATION NUMBER: US/0 FILING DATE: CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                   COUNTRY: US
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                                                                                                                                                                                                                                          CITY: Menlo Park
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
Sherwood,
                                                                                                                                                                                                                          USA
                                                                                                                                                                Floppy disk
                                                                        US/08/748,59
                                                                                                             Version
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEPAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Matches
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Local Similarity 70.9%;
les 630; Conservative
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                                                                        CTGAGAGCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCC
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                                           AAGAAGGTCTTCTACGTGATCGAGACGCGGGGAGCCGCGAGCGCCTGCTGCTCACCGCC
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Pred. No. 1.3e-91;
0; Mismatches 253;
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ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06510
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1576 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA.
US-08-748-591-10
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Epstein, Ervin
APPLICANT: Hu, Zhilan
APPLICANT: Bonifas, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1013 TCCTCGGGCTCGGGGCCCCTTCCGGGGGCGCACTGGGGCCCTCGGGCGC
416 GAAGAAAACACCGGAGCGGACAGGCTGATGACTCAGAGGTGTAAGGACAAGTTGAACGCT
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CITY: Menlo Park
STATE: CA
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                              90 CIGGICCIGITGCIGCIGGIGGIGGIGCCCGCGGCAIGGGGCTGCGGGCCCGGGTCCGGGTC 149
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                                                                                                                                            CCCAATGTGGCCGAGAAGACCCTAGGCGCCAGCGGAAGGTATGAAGGGAAGATCTCCAGA 355
                                   GAGGAGAACACAGGCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCG 389
                                                                     630;
                                                                                                         AGCTCCGAGCGCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGAC 329
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Similarity 70.9%;
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           MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DETA:
APPLICATION NUMBER: US/08/176,427;
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                              APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
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ZIP: 02109
                                                                                                                                                                                                                                              CITY: Boston
STATE: MA
   REFERENCE/DOCKET NUMBER:
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Best Local
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TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base pairs
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                   TGAGAGCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCG
                                                                                     AGGATGGGAGCCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCCACAGGC
                                                                                                                                                                       GTGGGGCGCGTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGG
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Pred. No. 1.1e-88;
0; Mismatches 357;
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US-08-356-060A-4
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US-08-356-060A-4
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                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: MMI-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                              TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                        MOLECULE TYPE:
FEATURE:
                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base pairs
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CITY: BO
STATE: M
COUNTRY:
          NAME/KEY:
LOCATION:
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                                                                                   STRANDEDNESS:
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                                                                                                                   CATTIGCCAGCCAGCCAGCCIGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGC
                                                                                                                                                                                CTCACCTGCTCT---TTACGGCTGACAATCACACGGAGCCGGCAGCCCGCTTCCGGGCCA 927
                                                                                                                                                                                                                          TGAGAGCCTTCCAGGTCATCGAGACTCAGGACCCCCCACGCCGCCTGGCACTCACACCCG
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 CGTACGCGCCCCACGGCACGGCACCATTCTCATCAACCGGGTGCTCGCCTCGTGCT
                                                                                                    TCTTTGCCAGCCGCGTGCGCCCCGGGCAGCGCGTGTACGTGGTGGCTGAACGCGGCGGGG
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                                                  AGCCTGCCCGCGTGGCAGCTGTCTCTACACACGTGGCCCT---
                                                                                                                                                                                                                                                                                      AGGATGGGAGCCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCCACAGGC
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04; Conservative
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; NAME/KEY: LOCATION: PCT-US95-02315-1
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                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 706; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1715 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORIX/AGENT INFORMATION:
ATMAC: John P. White
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4537
TELECOMMUNICATION INFORMATION:
TELEBHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROELINK, HENK APPLICANT: EGIUNG, Thomas TITLE OF INVENTION: DAMA ENCITITLE OF INVENTION: HEDGEHO TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1185 AVEL
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
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ADDRESSEE: Cooper &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1049
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                      463
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                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                             91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC 1154
                                     TGGTCCTGTTGCTGCTGGTGGTGCCCGCGGCATGGGGCCTGCGGGCCGGGTCGGGTGG 150
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                                                                                                   TGGGCAGCCGCCGGCGACACCGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGCC
                                                                                                                                             TGGCCCTTGCTTCCTCGCTGCTGGTGTGCCCCCGGACTGGCCCTGTGGGCCCCGGCAGGGGGT 405
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                     CCAACGTAGCCGAGAAGACCCTAGGGGCCCAGCGGCCGATATGAAGGGAAGATCACAAGAA
                                                                                 TTGGAAAGAGGCAGCACCCCAAA---AAGCTGACCCCTTTAGCCTACAAGCAGTTTATCC
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1185 Avenue of the
                                                                                                                                                                                                            Conservative
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 Sequence 3, Application US/08176427B Patent No. 5789543
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: MCMAhon, Andrew P.
APPLICANT: Tabin, Clifford J.
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Ingham, Phillip (
McMahon, Andrew )
Tabin, Clifford
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REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1190 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 63.0 Matches 665; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION DATA:
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                        520 ACCGCGACCGCAATAAGTATGGACTGCTGGCGCGCTTTGGCAGTGGAGGCCGGCTTTGACT
                                                                                                                                                                                                                                                            340 CAGGCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGCTATCT 399
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STRANDEDNESS: both
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                                                                                      GCCACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGGTGGACATCACCACATCAG
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Pred. No. 1.7e-84;
0; Mismatches 387;
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APPLICATION NUMBER: US/08,
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 30-DEC-1993
                                                                                                                                                                                    ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto **
NUMBER OF SEQUENCES: 47
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1058
                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                MA
USA
                                                                                                                                                                                                                                                                                                                     60 State Street
                                                                                                                                                                                                                                                                                                                                          LAHIVE & COCKFIELD
UMBER: US 08/176,427
30-DEC-1993
                                                                                                    US/08/356,060A
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; NAME/KEY: ; LOCATION: US-08-176-4278-3

MOLECULE TYPE: FEATURE:

TOPOLOGY:

Query Match

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1190 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 665; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Vincent, Matthew P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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STRANDEDNESS: both
TOPOLOGY: linear
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                                                        GCCCCACCTTCAGCGATGTGCTCATTTTCCTGGACCGCGAGCCCCACAGGCTGAGAGCCT 819
                                                                                                                                          GTGTGGCCTTGTCAGCCGTGAGGCCGGGAGACCGTGTGCTGGCCATGGGGAGGATGGGA 759
                                                                                                                                                                                                                   CAGCCAAGACGGGCGGCTGCTTCCCTGCCGGAGCCCCAGGTACGCCTGGAGAGTGGGGCGC
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                                   GAGTGGTACCCACGCCAGTGCTGCTCCTTCCTGGACCGGGATCTGCAGCGCCGCGCCTCGT
                                                                                                                                                                               CGGTCCGAGCCGGAGGCTGCTTTCCGGGAAATGCCACGGTGCGCTTGCGGAGCGGCGAAC
                                                                                                                                                                                                                                                      GGGTCTACTACGAGTCCCGCAACCACCATCCACGTATCGGTCAAAGCTGATAACTCACTGG
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Best Local Similarity

25.8%;

Score 418.2; DB Pred. No. 4e-84;

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Length

Query Match

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; NAME/KEY:
; LOCATION:
US-08-176-427B-9
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US-08-176-4278-9
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                                                                                                                                                                                                                                                                                                                             ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,427;
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
                                                                                                                                          TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1256 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                       MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                    TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATTHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1120 CTCAGTTGGCCTTTGGCCCCTGAGACTCTTTCAC 1154
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                                                                                       TOPOLOGY:
                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: MA
                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCAGCTGTCTCTACACACGTGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCATGGGA 1059
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30-DEC-1993
N: 475
                                                                                                            both
                                                                                                                                                                                                   7) 227-7400
227-5941
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ATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGACGACGACGACC 464
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                                                                                                                                                                                                                                                                                           CAGCCTGGCCAGTACGTGCTGGTGGCTGGGGTGCCAGGCCTGC---AGCCTGCCGCGTG 1001
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                                                                                ATTGTGGTCGACAGAATACTGGCGTCCTGTTACGCCGTAATAGAGGACCAGGGGCTTGCG
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent Matthew P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1256 base pairs
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APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
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APPLICATION NUMBER: US/08/356,060A
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COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 63.4%;
les 674; Conservative
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TOPOLOGY: lir
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ZIP: 02109
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                                                              AAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACACAGGC 344
                                                                                                                  AAGACCTTAGGGGCCAGCGGCAGATACGAGGGCAAGATAACGCGCAATTCGGAGAGATTT 219
                                                                                                                                          AGACATCCGAAGAAGCTGACACCTCTCGCCTACAAGCAGTTCATACCTAATGTCGCGGAG 159
                                         AAAGAACTTACTCCAAATTACAATCCCGACATTATCTTTAAGGATGAGGAGAACACGGGA
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60 State Street
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Pred. No. 4e-84;
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Search completed: June 5, 2000, 07:56:48 Job time: 3779 sec

Run

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Title:

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Maximum DB seq length: 0
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Sequence:
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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Gapop 10.0 , Gapext 1.0
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increasing the survival of neuronal, dopaminergic and GABA-nergic cells - by using a ptc therapeutic such as a protein kinase inhibitor, or an agent derived from hedgehog polypeptides, useful in the treatment of parkinson's disease

Disclosure; Page 95-97; 138pp; English.

This nucleotide sequence comprises a coding region for the human comprises and protective agents in the treatment and prophylaxis of neurodegenerative disorders constituting from the loss of dopaminergic and/or GABA-nergic neurons, cor the general loss of tissue from the substantia nigra.

Exemplary disorders include Parkinson's disease, Huntington's disease (both claimed), amyotrophic lateral sclerosis and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene therapy constructs e.g. constructs encoding recombinant hedgehog polypeptides and trans-activation
                                                                                                                                                                                                                                                                                                                                                                         04 FEB-1999.
24-JUL-1998; U15419.
24-JUL-1997; US-900220.
(ONTO-) ONTOGENY INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Indian hedgehog (Ihh) cDNA.

Indian hedgehog; Ihh gene; human; dopaminergic; GABA-nergic; ptc therapeutic; patched; signal transduction; Parkinson's dHuntington's disease; amyotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                         P-PSDB; W97763.
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Human Indian hedgehog protein Ihh cDNA.
Indian hedgehog; Ihh gene; human; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle a
cachexia; muscular myopathy; myoblastic sarcoma; therap
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                                    Location/Qualifiers 51. .1286 /*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PT A new method to regulate muscle growth
Disclosure; Page 104-106; 130pp; English.
CC Indian hedgehog protein ihh (see Y05516). The invention relates to
CC Indian hedgehog protein ihh (see Y05516). The invention relates to
CC tissue by ecotopically contacting muscle cells, especially muscle
CC tissue by ecotopically contacting muscle cells, especially muscle
CC tissue by ecotopically contacting muscle cells, especially muscle
CC therapeutic (i.e. hedgehog proteins and gene therapy
CC constructs) or ptc therapeutic (i.e. a small organic molecule that
CC minics the effect of hedgehog proteins on patched signalling, or
CC constructs or potentiates patched signalling) in an amount effective
CC to alter the growth state of the treated cells. Also claimed is a
CC method for treatment or prevention of disorders of, or surgical or
CC commetic repair of, such muscle tissues, by administering a
CC muscle atrophy, in particular skeletal muscle atrophy or cardiac
CC muscle atrophy, cachexia, or muscular myopathy (all claimed). The
CC meyblastic-derived tissue to provide treatment of hyperblastic or
CC meyblastic growth of muscle tissue such as in myoblastic sarcoma
CC (also claimed). The hedgehog therapeutic preferably comprises at
CC (also claimed). The hedgehog therapeutic preferably comprises at
CC (also claimed) a human hedgehog gene.

Sequence 1622 BP; 277 A; 549 C; 510 G; 286 T;
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Best Local Similarity
Matches 1622; Conserv
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29-AUG-1997; US-057334.
(ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hi
WPI; 99-243557/20.
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TGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACCGCGACCGCAATAAGTATG
                 TGCATTATGAGGGCCGCGCGGTGGACATCACCACATCAGACCGCGACCGCGATAAGTATG
                                                       ATTACAATCCAGACATCATCTTCAAGGACGAGGAGAACACAGGCGCCGACCGCCTCATGA 360
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1620 1620	1561 CTCAGCCTGCTCTACTACGAGTTTTCATACTCTGCCTCCCCATTGGGAGGGCCCATTC	DB Qy
1560 1560	1501 AGGGGATGGTTGTTGACCCCTCTCTCCTAGAGACCTTGAGGCTGGCACGGCGACTCCCAA	Qy
1500 1500	1441 AACACCAGCGTCCCCCACCCGGGTCGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGGGG	Фр
1440 1440	1381 GGACACTGGCTCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGC	Оу
1380 1380	1321 ACTGGGTCCAGAAGCCTCTCAGCCAGGAGGGAGCTGGCCCTGGAAGGGACCTGAGCTGGG	ДУ
1320 1320	1261 TGGGCATGTCCGGGGCAGGGAGCTGAAAGGACTCCACCGCTGCCCTCCTGGAACTGCTGT	Оу
1260 1260	1201 ACCCCCAGCTGCTCTACCGCCTGGGGGGGTCTCCTGCTAGAAGAGGGCAGCTTCCACCCAC	Оy
1200	1141 TGAGACTCTTTCACAGCTTGGCATGGGGCAGCTGGACCCCGGGGGAGGGTGTGCATTGGT	Οу
1140 1140	1081 TGGCATCCTGCTTCGCGGCCGTGGCTGGCCACCTGGCTCAGTTGGCCCTTCTGGCCCC	Qу
1080	1021 TGGCCCTCGGGGCCTACGCCCCGCTCACAAAGCATGGGACACTGGTGGTGGAGGATGTGG	Qy Db
1020	961 TGCTGGTGGCTGGGGTGCCAGGCCTGCAGCCTGCCCGCGTGGCAGCTGTCTCTACACACG	g Qy
960	1 CGGAGCCGGCAGCCCGCTTCCGGGCCACATTTGCCAGCCA	Db Qy
900	841 ACCCCCACGCCGCCTGGCACTCACACCCGCTCACCTGCTCTTTACGGCTGACAATCACA 	Qy
840	781 TCATTITCCIGGACCGCGAGCCCCACAGGCIGAGAGCCTTCCAGGTCATCGAGACTCAGG	g Qy
780 780	721 GGCCGGGAGACCGTGTGCTGGCCATGGGGGAGGATGGGAGCCCCACCTTCAGCGATGTGC	Db Qy
720 720	661 TCCCTGCCGGAGCCCAGGTACGCCTGGAGAGTGGGGCGCGTGTGGCCCTTGTCAGCCGTGA	Qу
660	601 CCCACGTGCATTGCTCCGTCAAGTCCGAGCACTCGGCCGCAGCCAAGACGGGCGGCTGCT	Qy db
600	541 GACTGCTGGCGCGTTGGCAGTGGAGGCCGGCTTTGACTGGGTGTATTACGAGTCAAAGG	Qу

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1621 CC 1622

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Pressis; w94470.

Pressis; w94
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Best Local Similarity
Matches 1129; Conser
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07-JAN-1999, U13387.
26-JUN-1997, US-883656
(ONTO-) ONTOGENY INC.
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X16184;
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Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell;

Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell;

brain infarction; cerebral infarction; transient ischaemic attack;

stroke; cerebral infarct volume; spinal cord; oedema; trauma;

haemorrhage; encephalomyelitis; coronary bypass; cerebral hypoxia;
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Key
CDS
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WPI; 99-095458/08.
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nilarity 88.4%;
Conservative
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US-883656.
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Pred. No. 2.9e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PT increasing the survival of neuronal, dopaminergic and GABA-nergic recells - by using a ptc therapeutic such as a protein kinase inhibitor, or an agent derived from hedgehog polypeptides, useful in the treatment of Parkinson's disease

PS Disclosure; Page 87-89; 138pp; English.

This nucleotide sequence includes a coding region for the mouse in the treatment and grophylaxis of neurodegenerative disorders resulting from the loss of dopaminergic and/or GABA-nergic neurons, or the general loss of tissue from the substantia nigra.

CC in the general loss of tissue from the substantia nigra.

CC disease (both claimed), amyotrophic lateral sclerosis and cerebral schease (both claimed), amyotrophic lateral sclerosis and cerebral schease (both claimed), amyotrophic lateral sclerosis and cerebral constructs for altering hedgehog gene regulatory sequences) and ptc therapeutics (i.e. agents which minic the effect of naturally concurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. Human Inh and Dhh cocurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. Human Inh and Dhh cocurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. Human Inh and Dhh cocurring hedgehog proteins on patched signalling) that are animal. They can also be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in the provention and/or treatment of hypoxia, e.g. as a neuroperotective conditions and/or treatment of hypoxia, e.g. as a neuroperotective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63. Best Local Similarity 88. Matches 1129; Conservative
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Mouse Indian hedgehog (Ihh) cDNA.

Mouse Indian hedgehog; Ihh gene; mouse; dopaminergic; GABA-nergic;
ptc therapeutic; patched; signal transduction; Parkinson's d
Huntington's disease; amyotrophic lateral sclerosis;
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Mahanthappa NK, Miao N, Pang
WPI; 99-142578/12.
P-PSDB; W97767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Problem without to regulate muscle growth
Disclosure; Page 96-98; 130pp; English.
CC This nucleotide sequence comprises a coding region for the mouse
CC Indian hedgehog protein Inh (see Y05512). The invention relates to
CC tambian hedgehog protein Inh (see Y05512). The invention relates to
CC tissue by ecotopically contacting muscle cells, especially muscle
CC tissue by ecotopically contacting muscle cells, especially muscle
CC tissue by ecotopically contacting muscle cells, especially muscle
CC therapeutic (i.e. hedgehog populations and gene therapy
CC constructs) or ptc therapeutic (i.e. a small organic molecule that
CC minics the effect of hedgehog proteins on patched signalling, or
CC activates or potentiates patched signalling) in an amount effective
CC to alter the growth state of the treated cells. Also claimed is a
CC method for treatment or prevention of disorders of, or surgical or
CC commetic repair of, such muscle tissues, by administering a
CC muscle atrophy, in particular skeletal muscle atrophy or cardiac
CC muscle atrophy, cachexia, or muscular myopathy (all claimed). The
CC myoblastic growth of muscle tissue to provide treatment of hyperblastic or
CC method polypeptide or ptc therapeutic can inhibit growth of
CC myoblastic derived tissue to provide treatment of hyperblastic or
CC method for muscle tissue such as in myoblastic sarcoma
CC (also claimed). The hedgehog therapeutic preferably comprises at
CC (clastic abloactive extracellular portion of a hedgehog protein (see
CC 905510-19) encoded by a vertebrate hedgehog gene (see X25098-107),
CC especially a human hedgehog gene.

Sequence 1281 Bp; 229 A; 401 C; 393 G; 258 T;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 1129; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ONTO-) ONTOGENY INC.
Bladgen CS, Currie PD, Hughes SM, Ingham
WPI; 99-243557/20.
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04-MAR-1999.
28-AUG-1998; U17922.
29-AUG-1997; US-057394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse Indian hedgehog prôtein Ihh cDNA.
Indian hedgehog; Ihh gene; mouse; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy; ds.
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     CGCCTCATGACCCAGCGCTGCAAGGACCGTCTGAACTCACTGGCCCATCTCTGTCATGAAC
                                                                  CTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGGAGAAACACAGGCGCCGAC
                                                                                                                                                   CTGGGCGCCAGCGGACGCTATGAAGGCAAGATCGCTCGCAGCTCCGAGCGCTTCAAGGAG
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; Pred. No. 2.9e-
0; Mismatches
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2.9e-194;
hes 147;
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   RESULT
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Human Indian hedgehog protein gene. Human; Indian hedgehog gene; nested polymerase
                                   Q91641;
18-MAR-1996
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                                                                   standard; cDNA;
                                   (first entry)
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Best Local Similarity
Matches 936; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence encodes a human Indian hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and has been isolated by screening of human genome DNA by nested polymerase chain reaction using primers Q91643, Q91644 and Q91645, followed by use of a clone to screen a human fetal lung 5'-stretch plus cDNA library in phage lambda gt-10. Probes and primers derived from hedgehog sequences may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the encoded protein may be used as therapeutic or research reagents.

Sequence 939 BP; 154 A; 305 C; 314 G; 166 T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hedgehog-like protein(s) and to treat degenerative nervous
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Pred. No.
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system disorder(s) and in gene
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Query Match
Best Local Similarity
Matches 928; Conser
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13-JUL-1995.
30-DEC-1994; U14992.
30-DEC-1994; US-376427.
14-DEC-1994; US-356060.
(HARD ) HARVARD COLLEGE.
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
Ingham PW, Mcmahon AP, Tabin CJ;
WPI; 95-255060/33.
P-PSDB; R77343.
                                                                 The sequence encodes a mouse Indian hedgehog protein, homologous to a prosophila hedgehog protein (R7737), and has been isolated by low stringency screening of a mouse genome DNA library and screening of an 8.5 day post coitum cDNA library. The partial cDNA is complete at the 3'-end, as evidenced by the presence of a polyadenylation consensus sequence and short poly-A tail. Probes and primers derived from hedgehog sequences may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the encoded protein may be used as therapeutic or research reagents.

Sequence 1056 BP; 204 A; 321 C; 312 G; 219 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Indian hedgehog protein gene.
Mouse; Indian hedgehog gene; probe; primer; diagnostic;
nervous system disorder; gene therapy; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1251
                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                             Hedgehog-like protein(s) and nucleic to treat degenerative nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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14-MAR-1996
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                                                                                                                  ACCCCGGGGGAGGGTGTGCATTGGTACCCCCAGCTCTACCGCCTGGGGCGTCTCCTG
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Best Local Sin
Matches 763;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 95-255060/33.
P-PSDB; R77338.
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30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
(HARD ) HARVARD COLLEGE.
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
Ingham PW, Mcmahon AP, Tabin CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus domesticus. W09518856-A1. 13-JUL-1995.
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Q91636;
22-FEB-1996 (first ent
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Claim 2; Page 133-35; 210pp;
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                                          GGGACCGCAGCAAGTACGGAATGCTGGCCCGCCCTCGCCGTCGAGCCGGCTTCGACTGGG
                                                                  GCGACCGCAATAAGTATGGACTGCTGGCGCGCTTGGCCAGTGGAGGCCGGCTTTGACTGGG
                                                                                                                                                   TGATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGAGGACGGCC
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Pred. No. 3.9e-82;
0; Mismatches 360
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                         WO9900117-A2.
07-JAN-1999.
26-JUN-1998: U13387.
27-JUN-1997: US-883656.
(ONTO-) ONTOGENY INC.
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Chicken Shh hedgehog cDNA sequence.
Chicken Shh hedgehog cDNA sequence.
Patched; hedgehog; ptc therapeutic; neuroprotective; neuronal cell; brain infarction; cerebral infarction; transient ischaemic attack; stroke; cerebral infarct volume; spinal cord; oedema; trauma; haemorrhage; encephalomyelitis; coronarv humann.
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DR P-SDB; W94468.

DR Method for limiting damage to neurons caused by ischaemic or epoxic productions - is used for the treatment and prevention of e.g. conditions - is used for the treatment and prevention of e.g. Productions - is used for the transient ischaemic attacks proceed at infarction, stroke and transient ischaemic attacks proceed at the provide and transient ischaemic attacks.

CC bischaemic or epoxic conditions by administering a ptc (patched) concurrent cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this construct which recombines with the genomic hedgehog gene to provide a construct of the ptc therapeutic agent is used to protect corbital tissues against ischaemic linjury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic conditions may also be used as a prophylactic in many qther cases of conditions may cause cerebral hypoxia, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. Creatment (which may be prophylactic) is used where ischaemic/epoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypotension. The treatment reduces CIV by at least 25, particularly at least 70,8. The company is a hedgehog sequence given in the present
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Length 1277; Indels

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Increasing the survival of neuronal, dopaminergic and GABA-nergic cells - by using a ptc therapeutic such as a protein kinase rinhibitor, or an agent derived from hedgehog polypeptides, useful in the treatment of Parkinson's disease bisclosure; Page 83-85; 138pp; English.

This nucleotide sequence comprises a coding region for the chicken Sch Sonic hedgehog protein (see W97765). The invention is based on the finding that hedgehog proteins are useful as protective agents in the treatment and prophylaxis of neurodegenerative disorders cresulting from the loss of dopaminergic and/or GABA-nergic neurons, or the general loss of tissue from the substantia nigra.

Exemplary disorders include Parkinson's disease, Huntington's disease (both claimed), amyotrophic lateral sclerosis and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene therapy constructs e.g. constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken Sonic hedgehog (Shh) cDNA.
Chicken Sonic hedgehog (Shh) cDNA.
Sonic hedgehog; Shh gene; chicken; dopaminergic; GABA-nergic;
ptc therapeutic; patched; signal transduction; Parkinson's disease;
Huntington's disease; amyotrophic lateral sclerosis;
cerebral ischaemia; hypoxia; neuroprotective; gene therapy; ss; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-1998; U15419.
24-JUL-1997; US-900220.
(ONTO-) ONTOGENY INC.
                                                                                                                                                                                                                                                                                                                                                                   WPI; 99-142578/12.
P-PSDB; W97765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus domesticus.
WO9904775-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructs for altering hedgehog gene regulatory sequences) and ptc therapeutics (i.e. agents which mimic the effect of natural
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ct issue by ecotopically contacting muscle cells, especially especia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A new method to regulate muscle growth Disclosure; Page 92-94; 130pp; English and the chicken This nucleotide sequence comprises a coding region for the chicken Sonic hedgehog protein Shh (see Y05510). The invention relates to a method for modulating the formation and/or maintenance of muscle a method for modulating the formation and/or maintenance of muscle
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28-AUG-1998; U17922.
29-AUG-1997; US-057394.
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Sonic hedgehog; Shh gene; chicken; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy; ds.
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WPI; 99-243557/20.
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PT Increasing the survival of neuronal, dopaminergic and GABA-nergic process by using a ptc therapeutic such as a protein kinase with into the treatment of parkinson's disease

PT inhibitor, or an agent derived from hedgehog polypeptides, useful in process the treatment of Parkinson's disease

PS Disclosure; page 97-99; 138pp; English.

CC This nucleotide sequence comprises a coding region for the human combined that hedgehog protein (see W97764). The invention is based on the treatment and prophylaxis of neurodegenerative disorders combined that hedgehog protein sare useful as protective agents continued that hedgehog protein sare useful as protective agents continued that hedgehog protein sare useful as protective agents continued that hedgehog protein sare useful as protective agents continued that hedgehog proteins are useful as protective agents continued that hedgehog proteins are useful as protective agents continued that hedgehog continued the substantian nigra.

CC in the general loss of tissue from the substantian nigra.

CC disease (both claimed), amyotrophic lateral sclerosis and cerebral continued to the protects of central sclerosis and cerebral ischaese (both claimed), amyotrophic lateral sclerosis and cerebral continued protects and gene therapy constructs e.g. constructs constructs for altering hedgehog polypeptides and trans-activation concurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. A bloactive protective and both human and animal subjects. A bloactive conditions arising from the use conficient of treat neurodegenerative conditions arising from the use of certain drugs, and in the prevention and/or treatment of hypoxia, conficultive agent.
                                                                                                                                                                                   Query Match
Best Local S
Matches 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
WO9904775-A2.
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 GGCGACCGCCACGCA----AACTCGTGCCGCTCGCCTACAAGCAGTTCAGCCCCCAATGTGC
                                                                                                            TGGCACTTCTGGCGCTGCCAGCCCAGAGCTGCGGGCCGGGCCCGGGGGCCCGGTTGGCCGGC
                                    GCCGCTATGCGCGCAAGCAGCTCGTGCCGCTACTCTACAAGCAATTTGTGCCCGGCGTGC
                                                                                                                                                                                                         Similarity
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e 1190 BP; 176 A;
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0; Mismatches 407;
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PS Disclosure; Page 106-108; 130pp; English.
PS Disclosure; Page 106-108; 130pp; English.
PS This nucleotide sequence comprises a coding region for the human CC Desert hedgehog protein Dhh (see Y05517). The invention relates to CC a method for modulating the formation and/or maintenance of muscle CC tissue by ecotopically contacting muscle cells, especially muscle CC stem/progenitor cells, in vitro or in vivo, with a hedgehog CC therapeutic (i.e. hedgehog proteins on patched signalling, or CC constructs) or ptc therapeutic (i.e. a small organic molecule that CC mimics the effect of hedgehog proteins on patched signalling, or CC activates or potentiates patched signalling) in an amount effective CC to alter the growth state of the treated cells. Also claimed is a CC method for treatment or prevention of disorders of, or surgical or CC consettic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be compared atrophy, in particular skeletal muscle atrophy or cardiac CC muscle atrophy, cachexia, or muscular myopathy (all claimed). The hedgehog polypeptide or ptc therapeutic can inhibit growth of moscle tissue such as in myobiastic sarcoma CC (also claimed). The hedgehog therapeutic preferably comprises at CC (also claimed). The hedgehog therapeutic preferably comprises at CC (also claimed). The hedgehog therapeutic preferably comprises at CC (also claimed) a vertebrate hedgehog gene (see X25098-107), CC especially a human hedgehog gene.

SQ Sequence 1190 BP; 176 A; 375 C; 424 G; 215 T;
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Matches
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Bladgen CS, Currie PD, Hughes SM, Ingham
WPI; 99-243557/20.
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Desert hedgehog; Dhh gene; human; hedgehog therapeutic;
ptc therapeutic; patched; signal transduction; muscle atrophy;
cachexia; muscular myopathy; myoblastic sarcoma; therapy; ds.
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28-AUG-1998; U17922.
29-AUG-1997; US-057394.
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                                CCGTGATGAACATGTGGCCCGGAGTGCCCCTACGAGTGACTGAGGGCTGGGACGACGACGACG
                                                        CGGTGATGAACCAGTGGCCCGGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGACGACGA
                                                                                                                                                                 GCTTCAAGGAGCTCACCCCCAATTACAATCCAGACATCATCTTCAAGGACGAGAGAACA 339
GCCACCACTCAGAGGAGTCCCTGCATTATGAGGGCCGCGGGGGGACATCACCACATCAG
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Pred. No. 4.1e-81;
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           13-JUL-1995.
30-DEC-1994; U14992.
30-DEC-1993; US-176427.
14-DEC-1994; US-356060.
(HARD ) HARVARD COLLEGE.
  (HARD )
                                                                                                        Human; sonic hedgehog gene; nested polymerase chain reaction; fetal lung; probe; primer; diagnostic; nervous system disorde gene therapy; antibody; ss.
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                                                                             Homo sapiens.
WO9518856-A1.
                                                                                                       gene therapy; antibody;
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Q91639;
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to treat degenerative nervous system disorder(s) and in gene therapy.

Sclaim 2; Page 143-45; 210pp; English.

The sequence encodes a human sonic hedgehog protein, homologous to a Drosophila hedgehog protein (R77337), and has been isolated by screening of human genome DNA by nested polymerase chain reaction using primers O91643, Q91644 and Q91645, followed by use of a clone to screen a human fetal lung 5'-stretch plus cDNA library in phage to screen a human fetal lung 5'-stretch plus cDNA library by Clone has been isolated from a phage Pl library by Clone to samplified using primers SHHF (091654) and SHR (Q91655), to give clone SHHPl. A 2.5-kb EcoRI CA repeat fragment amplified using primers SHHCAF (Q91655) and SHCAR (Q91657).

Probes and primers derived from the sonic hedgehog sequence may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the encoded protein may be used as therapeutic or research reagents.

So Sequence 1425 BP; 249 A; 461 C; 506 G; 206 T;
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p-pSDB; R77341.
Hedgehog-like protein(s) and nucleic acid(s) encoding them -
to treat degenerative nervous system disorder(s) and in gene
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SULT 2 645932 CUS	N., DuBuque,1 M., Kucaba,T., Morris,M., Pa nberg,K., Soar pod,K., Wohldn	· 0 = 0	·
Qy 1133 CTGGCATGC          Db 299 CTGGAATGC	Catarrhini; Hominidae; Homo. G., Becker, M., Bonaldo, M.F., Chia	, 1 Pr	REFERENCE AUTHORS
Qy 1073 CCCCCTTGA           Db 241 CCCCCTTGA			KEYWORDS SOURCE ORGANISM
Qy 1013 ATGTCCTGG	3 3' Similar to TR:G443942 G443942 DESERT HEDGEHOG;, mRNA sequence. GI:1558743	GE:52554 CURSOR. 64660 64660.1	ACCESSION VERSION
Qy 953 GGGAGGAAG          Db 121 GGGAGGAAG	EST (#937208) Homo	AA064660 3:	RESULT 1 AA064660 LOCUS DEFINITION
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TITLE
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AI645932 537 bp mRNA EST 29-APR-1999 mullg06.yl Soares_thymus_2NbMT Mus musculus cDNA_clone IMAGE:639130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.3%; ilarity 91.3%; Conservative
                                                                                                                                                   GCATT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Organism="Homo sapiens"
//db_xref="GDB:3916972"
//db_xref="GDB:3916972"
//db_xref="Taxon:9606"
//clone=lib="Stratagene pancreas (#937208)"
//lab_host="SOUR cells (Kanamycin resistant)"
//lab_host="Sour cells (Kanamycin resistant)"
//note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
/note="Organ: pancreatic vector: pBluescript SK-; Site_1:
/note="Organ: pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTT 3'"
31 a 100 c 117 g 55 t 11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 t Length: 862 Std Error: 0.00 rimer: -40M13 fwd. from Amersham quality sequence stop: 283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone is available royalty-free through LLNL; contact the Consortium (info@inage.llnl.gov) for further information. ble reversed clone: similarity on wrong strand ble reversed clone: polyT not found t Length: 862 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : est@watson.wustl.edu
NG: There is evidence that suggests that the 384-well parent
of this clone contains both human and mouse derived clones.
the origin of this clone is uncertain. This caution should in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ngton University School of Medicine
Forest Park Parkway, Box 8501, St. Louis, MO 63108
314 286 1800
314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                   GCCTCTTGCTACGCGGTTCTGGAGAGTCACCAGTGGGCGCACCGCGCTTTTG
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                                                                                                                                                                                                                      CATT 1144
                                                                                                                                                                                                                                                                          AGACTGCTGCACGCGCTAGGGGC-NTGCTCCCGGC-GGGCCGTCCAGCCGA
                                                                                                                                                                                                                                                                                                                               AGACTGCTGCACGCGCTAGGGGCGCTGCTCCCCGGCGGGCCCGTCCAGCCGA 1132
                                                                                                                                                                                                                                                                                                                                                                                    GCCTCTTGCTACGCGGTTCTGGAGAGTCACCAGTGGGCGCACCGCTTNTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 254; DB 28;
Pred. No. 2.8e-40;
0; Mismatches 25;
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ORIGIN
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Best Local Similarity 86.8
Matches 263; Conservative
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                                  241
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                                                                                                                                                       181
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TACAACCCCGACATCATCTTCAAGGATGAGGAGACAGTGGAGCCGACCGCCTGATGACC
                                                                                                                                                                                                                                                                                                                                  GTGCCGCTACTACAAGCAATTTGTGCCCGGCGTGCCAGAGCGGACCCTGGGCGCCAGT 180
                                                                                                                                                                                                                                                                                                                                                                                              CAGAGCTGCGGGCCGGGGGGGGGGCGGTTGGCCGGCGCTATGCGCGCAAGCAGCTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCCTCTCCTGACCAATCTACTGCCCTTGTGCTGCCTTGGCACTTCTGGCGCTGCCAGCC 60
                                                                                                                                                       GGGCCAGCGGAGGGGAGGGTGGCAAGGGGCTCCGAGCGCTTCCGGGGACCTCGTGCCCAAC
                                                                                                                                                                                                             GTGCCTCTGCTATACAAGCAGTTTGTGCCCCAGTATGCCCCGAGCGGACCCTGTGCGCGAGT 414
                                                                                              GGGCCAGCGGAGGGGAACAAGGGGGGTCGGAGCGCTTCCGGGACCTCGTACCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5' similar to mRNA sequence.
A1645932
A1645932.1 GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the second contact of the second contact the seco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
On May 18, 1998 this sequence version replaced Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possible reversed cione: similarity on wrong strand Seq primer: -40RP from Gibco High quality sequence stop: 478.

Location/Qualifiers
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1 (bases 1 to 537)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:639130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares_thymus_2NbMT"
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2.6e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 537;
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                          Best Local Similarity 85.8 Matches' 260; Conservative
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                                                                        61 CAGAGCTGCGGGCCGGGGGCCGGGTTGGCCGGCGCCGCTATGCGCGCAAGCAGCTC 120
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CAGAGCTGCGGGCCGGGCCGAGAACCGGGTGGCCGNCGGCGTAATGTGCGCAAGCAACTT
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mullg06.x1 Soares_thymus_2NbMT
3' similar to TR:Q61488 Q61488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this ned
data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
On May 18, 1998 this sequence version
Other_ESTs: mullg06.y1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible reversed clone: similarity on wrong strand High quality sequence stop: 261.
Location/Qualifiers
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AI666359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Thymus"
//dev_stage="4 weeks"
//dev_stage="4 weekss"
//dev_stage="4 weeks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:639130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .463
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                                                                                                                                                                                                                                                                                      Score 234.8; DB 4
Pred. No. 1.6e-36;
0; Mismatches 43
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                                                                                                                                                                                                                                                                                                                                                                  DB 49;
                                                                                                                                                                                                                                                                                              43;
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DEFINITION
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Best Local S
Matches 220
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                                                                                                                        177 CAGTGGGCCAGCGGAGGGGAGGGTGGCAAGGGGCTCCGAGCGCTTCCGGGACCTCCTGCC 236
297 GACCGAGCGTTGCAAGGAGAGGGTGAACGCTTTGGCCATTGCCCGTGATGAACATGTGGCC 356
                                                                       237
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                                     61
                                                                                                                                                                                            Local Similarity
                                                                                                        TACAACCCCGACATCATCTTCAAGGATGAGGAGAACAGTGGAGCCGACCGCCTGATGACC 300
                                                                                                      CAGCGGGCGCTACTAAGGCAAAATCGCGCGCAGCTCTGAGCGCTTCAAGGAGCTCACCCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAG 161
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                                                                                                                                                                          220;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: nhiee@tigr.org
For clone availability, additional sequence and expression
information related to this EST please check the TIGR Rat (
Index (http://www.tigr.org/tdb/rgi/rgi.html). To order a ci-
contact the ATCC (http://www.atcc.org/atcc.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research 9712, Medical Center Drive, Rockvi. Tel: (301)-838-3529
Fax: (301)-838-0208
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On Jun 5, 1998 thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 29)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quacker Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW144802 299 bp mRNA EST291975 Normalized rat embryo, RGICG52 5' end similar to Indian AW144802
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                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                78
                                                                                                                                                                                                                                                                       /Organism="Rattus sp."
/db_xref="taxon:10118"
/db_mref="taxon:10118"
/clone="RGICG52"
/clone_lib="Normalized rat embryo, Bento Soares"
/clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
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                                                                                                                                                                          0;
                                                                                                                                                                                          Score 172.6; DB 6
Pred. No. 1.7e-24;
                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  washU Zebrafish EST Project 1998
Unpublished (1998)
On Jun 5, 1998 this sequence version replaced gi:3188836.
Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
1 (bases 1 to 406)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Lou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible reversed clone: similarity Seq primer: T3 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: zbrafish@watson.wustl.edu
stage embryos"
/lab_host="XL1-blue MRF"
                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Zebrafish WashU MPIMG/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                             /tissue_type="26 somite embryos, adult livers, shield
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EST Danio rerio cDNA 5' similar to
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embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
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                                            Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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AL066742.1
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACR14B09 of BCI-98 library from Drosophila melanogaster (fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Location/Qualifiers
1. .932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1405079.
On Sep 12, 1996 this sequence version replaced gi:1405079.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@manage.llnl.gov) for further information.
Insert Length: 615 Std Error: 0.00
Seg primer: -40m13 Fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                              AI015155 459 bp mRNA EST 27-AUG-1998 ot70h05.sl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622169 3' similar to TR:Q98938 Q98938 INDIAN HEDGEHOG
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 459)
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                                                                                                                                                                                                                                                                                                                                                                             PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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/clone_"lb="RPCI-98"
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202 c 241 g
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/db_xref="taxon:7227"
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                                                                                                        - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                              Eukaryota; Metazoá; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
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- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDG)
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCCCGTGTGGCGCGGGAGGAAGCCGTGGGGCGTGTTCGCGCCGCTC--ACCGCGCACGG 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTACGCGCTGGGGACTCGGTGCTGGCGCCCGGCGGGGATGCGCTTCGGCCAGCGCGCG 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTSSGSGYGKGCSSGSGBSCSCCSSCSSSSCSCCBCCCCCSCSSYCCSSSBSSSKC 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVGTSSSSDSTSTCCSCCCYMCTCCSTYBMBCYTSTSCGGSSSSSGKGGVTKCGCGGCGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSSSTSSBBSCTSTSSSSSSSSSSSSSTCSCCTCCCSYSYSSSTSSSSSTSWGSTSGSSSS 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGCTGCTGGTGAACGATGTCCTGGCCTCTTGCTACGCGGTTCTGGAGAGTCACCAGTG 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSKSTSASGSGSWSAGGGSGSTGSTSSSSSSSSTSTSSSSVSSGSKSSTBSSGSBSSSGS 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 512)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuc Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

Waterston, R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                         my52c03.rl Barstead clone IMAGE:699460
                                                                                                                                                                                                                                                                                                                                                                                                        AA245525
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                                                                                                                                                                                                                                                                                                             AA245525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-98"
/clone="BACR19D16"
/note="end : TET3"
a 61 c 61 g
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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15.5%; Pred. No. 0.
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5' similar to
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hes 132;
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                                                                                                                                                                                                                                                                                                                                CACGGGACGCTGCTGGTGAACGATGTCCTGGCCTCTTGCTACGCGGTTCTGGAGAGTCAC
                                                                                                                                                                                                                                CATCTGGCTCAGTTGGCCTTCTGCCCTGCGA 299
                                                                                                                                                                                                                                                                                                       CATGGGACACTTGTGGTGGAGGATGTGGTGGCCTCCTGCTTTGCAGCTGTGGCTGACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGCGCCGGCTACGCGCTGGGGACTCGGTGCTGGCGCCCGGCGGGGATGCGCCTTCGGCCA 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCTGCTCTTCATTGCGGACAATCATACAGAACCAGCAGCCCACTTCCGGGCCACATTT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144;
                                                                                               AI325370 452 bp mRNA EST 23-DEC-1998 m134b11.y1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE: 65405 5' similar to TR:Q61724 Q61724 INDIAN HEDGEHOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:693301.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                 PROTEIN ;, mRNA sequence. AI325370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -28m13 rev2 ET from
High quality sequence stop: 511.
Location/Qualifiers
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Fax: 314 286 1810
Mus musculus
                                                  AI325370.1
                house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:699460"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DH10B"
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                                                  GI:4059799
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Pred. No. 0.00044;
0; Mismatches 127
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                                                                                                                                                                                                                                                                 898 GIGCIGGCGCCCGGGGGAIGCGCTTCGGCCAGCGCGCGTGGCCCGTGTGGCGCGGGAG 957
181 CTGCGACTGTTTCCC 195
                                                                                                                                                                                                                                                                                                        hes 115;
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                     TTGAGACTGCTGCAC 1092
                                                                                                CIGGCCICIIGCTACGCGGTICIGGAGAGICACCAGIGGGGGCGCACCGCGCIIITIGCCCCC 1077
                                                                                                                                                  GTGGCCCTTGGGTCCTATGCTCCTCTCACAAGGCATGGGACACTTGTGGTGGAGGATGTG 120
                                                                             GTGGCCTCCTGCTTTGCAGCTGTGGCTGACCACCATCTGGCTCAGTTGGCCTTCTGGCCC
                                                                                                                                                                                       GAAGCCGTGGGCGTGTTCGCGCCCCCCCCCCCCCCCGCGCACGCTGCTGGTGAACGATGTC 1017
                                                                                                                                                                                                                             Unpublished (1996)
on Jan 19, 1998 this sequence version replaced gi:215229
Contact: Maxira W. Mouse EST Project
washU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu. Geisel, S., Kucaba, T., Lacy, M., Le, M., Wartin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
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Seq primer: -40RP fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the {\tt IMAGE} Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                        Similarity
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314 286 1810
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                             mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="057BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:465405"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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Rođentia;
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                                                                                                                                                                                                                                                                                                    Score 67; DB 44; L
Pred. No. 0.00061;
""amatches 80;
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958 CAAGCCGTGGGCGTGTTCGCGCCCCCCCCCCCCCCGCGCACGCTGCTGCTGCAACGATGTC 1017

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REFERENCE
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                                898 GTGCTGGCGCCGGGGGATGCGCTTCGGCCAGCGCGCGTGGCCCGTGTGGCCGCGGGAG 957
                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
On Nov 29, 1993 this sequence version replaced g1:
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     m134b11.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:465405 5' similar to PIR:C49425 C49425 Indian hedgehog protein - mouse ;, mRNA sequence.

AA032692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: similarity on wrong strand Seq primer: -28M13 rev2 from Amersham
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Eutheria; Rodentia;
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                                                                                                                                                                                  49
                                                                    Conservative
                                                                                                                                                                                                   M.Fatima Bonaldo.
100 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:465405"
                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                      58.5%;
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                                                                    0
                                                                                      Score 65.4; DB 2
Pred. No. 0.0011;
                                                                      Mismatches
                                                                                                                                                                                  79
                                                                                                     27;
                                                                                                       Length 324;
                                                                    Indels
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Mus.
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REFERENCE
AUTHORS
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CNS006XK/c
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Best Local S
Matches 123
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JOURNAL
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                                                                                                          864
                                                                                                                                         935 GGSCGGGGGGSGSSGSSGCGSGCGSGSGGSCCCCSGSCCCCSCSCSCSCSCSSSSCCC
                                                                                                                                                                          804 GCCCTGGCACCTGGTGTTTGCCGCTCGAGGGCCGGCGCCCCGCGCCAGGCGACTTTGCACC 863
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                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be coation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIGCGACIGITICCC
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CGCGCCGSCSCGCGCCGGCSGGCCSGGCGSSGCGGCSGCCGCSGKSKCGCGCGGS
                                                                                                      GGTGTTCGCGCGCCGGCTACGCGCTGGGGGACTCGGTGCTGGCGCGCGGGGG----GATG
                                  CGCTTCGGCCAGCGCGTGGCCCGTGTGGCGCGCGGAGGAAGCCGTGTGGGCGTGTTCGCGC 979
                                                                     BP
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 935)
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GSS.
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fr
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                                                                                                                                                                                                                                                                                                                /organism="Drosophila m
/db_xref="taxon:727"
/clone_lib="RPCI-98"
/clone_"BACR14N09"
/note="end : T7" .
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(E-mail : seqref@genoscope.cns.fr
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 953
                                 844 GCGCCAGGCGACTTTGCACCGGTGTTCGCGCGCCGGCTACGCGCTGGGGACTCGGTGCTG 903
                                                                                                     784 CCACGCAAACTGTTGCTCACGCCCTGGCACCTGGTGTTTTGCCGCTCGAGGGCCGGCGCCC 843
                                                                                                                                                                        724 TICCIGGACCGGGACTIGCAGCGCCGGGCTTCATTTGTGGCTGTGGAGACCGAGTGGCCT 783
                                                                     TBTSTSSSSTTTTTTTTTTTTTTSTTBTBBSSBSBSSSSSTSSSBBTSKSBTSBSSBSTSSS
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ASBSSSSSSSSSTSTTBSTSBBBSTSSSSSSSSSSSBBSTBSBSSBTBTTTTTBTKSTS
                                                                                                                                       AL108460.1
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             project grant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genevieve Payan.
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                               /clone_lib="DrosBAC"
/clone="BACN37L08"
/note="end : SP6"
a 176 c 160 g
                                                                                                                                                                                                                                                                                                                                                                                      /plasmid="pBeloBAC11"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila
/blasmid="bBeloBAC11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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15.6%;
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Pred. No. 0.0045;
06; Mismatches 18
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1040 TGGAGAGTCACCAGTGGGCGCACCGCGCTTTTGCCCCCCTTGAGACTGCTGCACGCGCTAG 1099
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                                                                                                                                                                  BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                            The DNA was prepared from embryos by Alain Bucheton Payan. It has been constructed in the vector
melanogaster"
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BASE COUNT
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703 GTGCCCACGCCGGTGCTGCTTCCTGGACCGGGGACTTGCAGCGCCGGGGCTTCATTTGTG 762
                                                                                              Local Sinhes 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr -

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC198 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order institutions in BAC clones the action of the library and how to order institutions in BAC clones the action of the library and how to order institutions in BAC clones the action of the library and how to order institutions in BAC clones the action of the library and how to order institutions in BAC clones the action of the library and how to order institutions in BAC clones the same strain was constructed.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 932)
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AL066742 AL066742.1 GI:4945205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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llarity 31.4%;
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14B09"
/note="end: T7"
/note="end: T7"
202 c 241 g 91 t 243
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                                                                                     Score 62; DB 8
Pred. No. 0.008
39; Mismatches
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0.0067;
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                         GTCCAGCCGACTGCCATGCA 1142
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                                                    CCCGCVSGCSCCSCSMSCCCCCGCASCVCAGCCMSAGCMGCGCCMCCCGCCASCGSCCSC
                                                                             CGCGCTTTTGCCCCCCTTGAGACTGCTGCACGCGCTAGGGGGCGCTGCTCCCCGGCGGGGCC
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Copyright (c) 1993 - 2000 Compugen Ltd.
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1 (bases 1 to 512)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                              AA245525 512 bp
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clone IMAGE:699460 5'
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Sciurognathi; Muridae; Murinae;
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CNS006ON
CNS016BR
CNS0052P
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5 z178b12.y

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3 z mu11906.y

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                      GGGACTCTAACCACTGCCCTCCTGGAACTGCTGTGCTGGATCCAAAGGCCTCCTCACCAG
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                                         AGGACTC-CACCGCTGCCTCCTGGAACTGCTGTACTGGGTCCAGAAGCCTCTCAGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free th
IMAGE Consortium (info@image.llnl.gov)
MGI:433020
Seq primer: -28ml3 rev2 ET from Amersha
High quality sequence stop: 511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Apr 14, 1993 this sequence version replaced gi:693301. Contact: Marra M/Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
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h quality sequence stop: 511.
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/db_xref="taxon:10090"
/clone="IMAGE:699460"
/clone_lib="Barstead mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="mixed"
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Pred. No. 6.9e-60;
D; Mismatches 71
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les 372; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Jan 19, 1998 this sequence version replaced Contact: Marra M/MOUSE EST Project WashU-HHMI Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:279221

This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 415.
Location/Qualifiers
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 452)
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Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="ftaxon:10090"
/clone="IMAGE:465405"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="unknown"
                                                    19.9%;
                                     0
                                   Score 323.2; DB 44
Pred. No. 3.9e-54;
0; Mismatches 63;
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                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: WashU-Merck EST Project
This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                           correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 390.
Location/Qualifiers
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On Dec 20, 1995 this sequence version replaced gi:1133383.
Other_ESTs: z178b12.x5
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Z178bL2.y5 Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:510719 5', mRNA sequence.
AI733725
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National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)
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/cione_lib="Stratagene colon (#937204)"
/tissue_type="tumor"
/cell_line="T94 carcinoma cell line"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:510719"
                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:3843214"
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                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammali;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 324)
1 (bases 1 to 324)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Düb;
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Mortis, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                          Waterston, R.
The MashU-HHMI Mouse EST Project
Unpublished (1996)
On Nov 29, 1993 this sequence version repl
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA032692 324 bp mRNA EST 22-AUG-1996 m134b11.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:465405 5' similar to PIR:C49425 C49425 Indian hedgehog Protein mouse; mRNA sequence.
                                                                                                                                   4444 Forest Park Parkway, Box 8501, St. Tel: 314 286 1800 Fax: 314 286 1810
                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA032692
AA032692.1
                    Possible reversed clone: similarity on wrong Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse
quality sequence stop: 98
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EST.
Eukaryots, Metazoa; Chordata; Craniata; Verte Eutheria; Rodentia; Sciurognathi; Muridae; Mu 1 (bases 1 to 29)
Lee, N. H., Glodek, A., Chandra, I., Mason, T.M., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (
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EST291875 Normalized rat
RGICG52 5' end similar to
AW144802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism≖"Mus musculus"
/strain="C57BL/6J"
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/dev_stage="13.5-14.5dpc total
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/clone="IMAGE:465405"
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                                                         Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
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Pred. No. 3.3e-40;
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The Institute for 9712, Medical Cen Tel: (301)-838-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
For clone availability, additional sequence and expression information related to this EST please check the TIGR Rat Gene Index (http://www.tigr.org/tdb/rgi/rgi.html). To order a clone contact the ATCC (http://www.atcc.org/atcc.html).
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 444)

Hillier,L. Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Chissoe,S., Dietrich,N., DuBuque,T., Le,M., Le,M., Le,N., Le,N., He,N., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Le,N.,
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2178b12.r1 Stratagene colon (#937204)
IMAGE: 510719 5', mRNA sequence.
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Generation and analysis of 280,000 human Genome Res. 6 (9), 807-828 (1996)
                                                         and Marra, M.
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/db_xref="taxon:10118"
/clone="RGICG52"
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/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
/note="Vector: pT7T3Pac 3te_1: EcoRI; Site_2: NotI"
/note="Vector: pT7T3Pac 49 t
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Pred. No. 2.2e
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                                                                           AW430605 291 bp
70323 MARC 4BOV Bos t
AW430605
AW430605.1 GI:696191
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1974 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 221.
Location/Qualifiers
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
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On Sep 12, 1996 this sequence version replaced
                                                 Bos taurus.
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Fax: 314 286 1810
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/tissue_type="tumor"
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/clone="IMAGE:510719"
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/db_xref="GDB:3843214"
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                                                                              GI:6961912
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Pred. No. 2.1e-36;
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Matches 254;
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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
                                                                                                               AA628967 753 bp mRNA EST 16-OCT-1997 af28h06.sl Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1033019 3', mRNA sequence.
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1 (bases 1 to 291)

Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: AGGADACAGCTATGACCAT
BACKWARD: GTTTCCCAGTACGACG
BACKWARD: GTTTCCCAGTACGACG
Plate: 37 row: N column: 8
Seq primer: ATTTAGGTGACACTATAG.
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Fax: 402 762 4390

Email: smitheemail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
On Mar 10, 1998 this sequence version replaced
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                  Homo sapiens
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Similarity 87.3%;
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92 c
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Library made from pooled tissue from day 20 and da
embryos."
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/lab_host="DH10B"
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/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        610 CGTCGTGGTGGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCT 551
                                                                                                                                                                                                                                                                       GTTTTCATACTCGTGCCTCCCCATTGGGGAGGGCCCATTCC
                                                                                                                                                                                                                                                                                                                                                                 CTCTCCTAGAGACCTTGAGGCTGGCACGGCGACTCCCAACTCAGCCTGCTCTCACTACGA
                                                                                    A1958076 406 bp mRNA EST 20-AUG-
fc90e01.y1 Zebratish WashU MPIMG EST Danio rerio cDNA 5'
TR:Q92008 Q92008 VHH-1 PRECURSOR ;, mRNA sequence.
A1958076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 474.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 753)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Karizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Tan,F., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. WashU.NCI human,EST Project
Danio rerio
                                            EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
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On Sep 12, 1996 this sequence version replaced gi:1407418
                       zebrafish
                                                                 A1958076.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host-"DH10B"
/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1033019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%;
96.8%;
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Pred. No. 8.4e-30;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geisel, G., Jost, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                      similar to
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;

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TITLE
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                                                                                                                                                                             Query Match
Best Local Similarity
Matches 224; Conser
      148
                                              215
                                                                                                                               155 CAGCCGCCGGCGACCGCCAAACTCGTGCCGCCTACAAGCAGTTCAGCCCCAA 214
                                                                                          88
TGTCGAGGAGAAGACCTTATGGGCCAGCGGCAGATACAAGGGCCATGATAACGCGCCAATTA 207
                                            CGGCAGACTAAGACATCCGAAGATGCTGACACCTCTCGTCTACAAGCGGTTCATACCTAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Waterston, R. and Wilson, R. Washu zebrafish EST Project 1998
Unpublished (1998)
On Jun 5, 1998 this sequence version replaced gi:3188836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: zbrafish@watson.wustl.edu

CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.
1 (bases 1 to 406)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: T3 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www.rzpd.de]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 406)
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                  were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="Zebrafish WashU MPIMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                  10.6%;
                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                Score 171.2; DB 63; Pred. No. 2.4e-24;
                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Louis, MO 63108, USA
                                                                                                                                                                             Indels
                                                                                                                                                                                                                       Length 406;
                                                                                                                                                                             0;
                                                                                                                                                                           Gaps
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Query Match Best Local Matches 17

Similarity

9.78; 96.18;

Score 158; DB 41; Pred. No. 9.8e-22; 0; Mismatches 5;

Indels

2

Gaps

Conservative

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REFERENCE
AUTHORS
TITLE
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AI015155/c
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VERSION
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ORIGIN
               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
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                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 CATCTATGTAATGAACCACTGGCCAGTCGTTAAGCTGCGTGTGACAGACGGCTGAGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                395 TATCTCGGTGATGAACCAGTGGCCCGGTGTGAAGCTGCGGGTGACCGAGGGCTGGGACGA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 GGAGAGATTGAAAGAACTTACTCCATATTACAATGCCGACATTATCTTTAAGGATGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 CGAGCGCTTCAAGGAGCTCACCCCCAATTACAATCCAGGCATCATCATCTTCAAGGACGAGGA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGACGGCCACCA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACGGCCACCA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAACACGGTAGCGGACAGGCTCATGACACAGAGATGCAAAGACAAGCTGATCTCGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACACAGGCGCCGACCGCCTCATGACCCAGCGCTGCAAGGACCGCCTGAACTCGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIO15155 459 bp mRNA EST 27-AUG-1998 ot70h05.s1 Soares_tottal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622169 3' similar to TR:Q98938 Q98938 INDIAN HEDGEHOG PROTEIN.; mRNA sequence.

AIO15155
                                                                                                                                                                                                                                                                                                                                                     Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 392.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        On Sep 12, 1996 this sequence version replaced gi:1405079 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 459)
                106
                                                                                                                                                                                                                                                                                                                                                                                                                        (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene Index
               þ
      /clone="IMAGE:1622169"
                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db xref="taxon:9606"
                                                                                                                                                                                                                                                          /db_xref="taxon:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Project (CGAP),
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SOURCE
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AI666359/c
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ORIGIN
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TITLE
                                                                                                                                     Query Match
Best Local
                                                                                                                   Matches
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163 GGCGACCGCCACGCA---AACTCGTGCCGCCTCGCCTACAAGCAGTTCAGCCCCAATGTGC 219
                                                       341
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21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2019 MRNA 463 bp mRNA 3/ similar to TR:Q61488 Q61488 DE mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCACTCTTGGCACTATCTGCCCCAGAGCTGCGGGCCGGGCCGAGAACCGGGTGGCCGNC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACAAGCAGTTCAGCCCCAATGTGCCCGAGAAGAACCCTGGGCGCCAGCGGACGCTATGAA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACAAGCAGTTCAGCCCCAATGTGCCCCGAGAAGACCCTGGGCGCCCAGCGGACGCTATGAA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
On May 18, 1998 this sequence version
Other_ESTs: mullg06.y1
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible reversed clone: similarity on wrong strand High quality sequence stop: 261.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                   7.4%;
Similarity 68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI666359.1 GI:4804713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 theria; Rodentia; (bases 1 to 463)
                                                                                                                 Conservative
                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento
                                                                                                                                                                                                                                                                                                                                                              Soares and M.Fatima Bonaldo."
124 c 138 g 113 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:639130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                             Score 119.4; DB 49; Length 463; Pred. No. 3.6e-14; 0; Mismatches 82; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 12-MAY-1999
Mus musculus cDNA clone IMAGE:639130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESERT HEDGEHOG HOMOLOG PRECURSOR ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replaced g1:3136856
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BASE COUNT
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SOURCE
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VERSION
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AI645932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 CCGAGCGGACCCTGGGCGCAGTGGGCCAGCGGAGGGGTAACAAGGGGGTCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 GCGGCGCAGACCGCCTGATGACAGAG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTTCAAGGAGCTCACCCCCAATTACAATCCAGCACATCATCTTCAAGGACGAGGAGAGAACA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI645932 537 bp mRNA EST 29-APR-1999 mullg06.yl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:639130 5; similar to TR:Q61488 Q61488 DESERT HEDGEHOG HOMOLOG PRECURSOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
(1997)
(Inpublished (1997)
(I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 537)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possible reversed clone: similarity on wrong strand Seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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AI645932
AI645932.1 GI:4724407
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                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 478
            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:639130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Thymus"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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Query Match Best Local Similarity

7.1%; 67.3%;

Score 115.6; DB 49; Pred. No. 2.1e-13;

Length 537;

. 76 .

Site\_1:

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RESULT 1
AA064660
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KEYWORDS
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 TGCTGCTGGTGGTGCCCGCGGCATGGGGCCTGCGGGCCGGGTCGGGTGGTGGGCAGCCGCC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGACCGCCACGCA---AACTCGTGCCGCCTCGCCTACAAGCAGTTCAGCCCCAATGTGC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGCGCAGACCGCCTGATGACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGAGCGGACCCTGTGCGCGAGTGGGCCCAGCGGAGGGGAGGGTAACAAGGGGGTCGGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCACTCTTGGCACTATCTGCCCAGAGCTGCGGGCCGGGCCGAGGACCGGTTGGCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 314)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Chissoe,S., Dietrich,N., Kucaba,T., Lacy,M., Le,M., Le,N.,
Hawkins,M., Hultman,M., Kucaba,T., Pange,C., Rifkin,L.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlflug,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 9, 1995 this sequence version rep. Contact: Wilson RK
Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zml3f08.sl Stratagene pancreas (#937208) Homo sapiens cDNA clo
IMAGE:525543 3' similar to TR:G443942 G443942 DESERT HEDGEHOG
PRECURSOR. ;, mRNA sequence.
                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further i Possible reversed clone: similarity on wrong strand Possible reversed clone: polyT not found Possible reversed clone: polyT not found Insert Length: 862 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                          WARNING: There is evidence that suggests that the 384-well parent plate of this Clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                            Seq primer: -40M13 fwd. from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 286 1800
314 286 1810
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                                                                                                                                                                                      quality sequence stop: 283.
                                                     /organism="Homo sapiens"
/db_xref="GDB:3916972"
/db_xref="taxon:9606"
/clone="IMAGE:525543"
/clone_lib="Stratagene pancreas (#937208)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1995 this sequence version replaced gi:802645
                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 bp
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                                                                                                                                                                                                                                                                                                                                       contact the
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                                                                                                                                        BP 191 91006 EVRY codex - FRANCE (E-mail: seqrefégenoscope.cns.fr

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecori digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCAGTGGGCGCACCGCTTNTTTGCCCCCCTTGAGACTGCTGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ bases 1 to 925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genome
BACR19D16 of RPCI-98 library fi
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a 100.c 117 g 55 t 11 others
  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGTGCCGCCTCGCCTACAAGCAGTTCAGCCCCAATGTGCCCGAGAAGACCCCTGGGCGCCA 240
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                                                                                                                                                                                                                                                                   Email: egreen@nhgri.nih.gov
Plate: 05 row: E column: 11
Seq primer: -21M13 (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 27
Tel: 3014020201
Fax: 301402473
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AA076750.1 GI:1836434
EST.
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7B05E11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA
Clone 7B05E11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L., Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D. 2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 288)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 7 (3), 281-292 (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eric D. Green
/Clone_lib="Chromosome 7 Fetal Brain cDNA Library"
/sex="female and male mixture"
/tissue_type="brain"
/dev_stage="pool of 9 week and 12 week"
/lab_host="E. coli strain DH5 alpha"
/note="Organ: brain; 'vector: paMPLO; CDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA
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61 c 61 g
                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="7805E11"
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                                                                   189
                                                                                                                                  129 CTAGTCCTCGTCTCCTCGCTGCTGGTATGCTCGGGACTGGCGTGCGGGACCGGGCAGGGGG 188
                                                                                                150 GTGGGCAGCCGGCGACCGCCACGCAAACTCGTGCCGCTCGCCTACAAGCAGTTCAGC 209
                                                                                                                                                          90 CTGGTCCTGTTGCTGCTGGTGCTGCCGGGCATGGGGCTGCGGGCCCGGGTCGGGTG 149
TTCGGGAAGAGGAGGCACCCCAAA---AAGCTGACCCCTTTAGCCTACAAGCAGTTTATC 245
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                    60
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87 c 95 g 44 t 2 others
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